

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:11:58 ; Search time 16.77 Seconds  
(without alignments)  
28.649 Million cell updates/sec

Title: US-09-825-144-15  
Perfect score: 34  
Sequence: 1 FPPPP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	57	2 S10782	salivary protein p
2	34	100.0	79	1 PJHUSB	proline-rich pepti
3	34	100.0	104	2 AB3634	hypothetical prote
4	34	100.0	127	2 AH3450	hypothetical prote
5	34	100.0	134	2 D84672	hypothetical prote
6	34	100.0	147	2 S37485	gene msg1 protein
7	34	100.0	181	2 S44765	C29E4.9 protein -
8	34	100.0	186	2 T50403	probable succinate
9	34	100.0	204	2 B86410	protein F3M18.20 l
10	34	100.0	212	2 S57330	cathelin-like anti
11	34	100.0	212	2 T47947	hypothetical prote
12	34	100.0	228	2 S40463	prophenin (PF-2) p
13	34	100.0	236	2 T45835	hypothetical prote
14	34	100.0	247	2 A45707	immediate-early R1
15	34	100.0	253	2 T17312	hypothetical prote
16	34	100.0	272	2 S24375	hypothetical prote
17	34	100.0	275	2 T02559	probable spliceoso
18	34	100.0	278	2 T04504	hypothetical prote
19	34	100.0	287	2 T01919	probable Ap2 domai
20	34	100.0	289	2 T52354	hypothetical prote
21	34	100.0	291	2 S33209	extensin-like prot
22	34	100.0	296	2 A36366	enhancer-binding p
23	34	100.0	297	2 A35914	transcription fact
24	34	100.0	303	1 TVHUTD	transforming prote
25	34	100.0	316	2 C84635	hypothetical prote
26	34	100.0	322	2 S09779	hypothetical prote
27	34	100.0	341	1 TVMSJD	transforming prote
28	34	100.0	341	2 JCA051	Jun-D protein - ra
29	34	100.0	347	2 A43815	transforming prote

30	34	100.0	362	2 T51464	RING-H2 zinc finge
31	34	100.0	376	2 T39454	hypothetical prote
32	34	100.0	381	2 B86175	protein F19P19.21
33	34	100.0	406	2 T28957	hypothetical prote
34	34	100.0	406	2 H84590	hypothetical prote
35	34	100.0	415	2 T00614	hypothetical prote
36	34	100.0	429	2 T06296	extensin-like prot
37	34	100.0	457	2 T35443	aminotransferase -
38	34	100.0	466	2 T11684	RVS167 protein hom
39	34	100.0	468	2 S44815	F44B9.4 protein -
40	34	100.0	500	2 H96570	hypothetical prote
41	34	100.0	503	2 T19319	hypothetical prote
42	34	100.0	507	2 C71412	probable hydroxypr
43	34	100.0	508	2 T21866	hypothetical prote
44	34	100.0	513	2 C81885	probable NAD(P)+ t
45	34	100.0	513	2 F81134	NAD(P) transhydrog
46	34	100.0	517	2 T49937	hypothetical prote
47	34	100.0	524	2 H97658	pyridine nucleotid
48	34	100.0	524	2 AB2883	NAD(P)+ transhydro
49	34	100.0	528	2 T52092	DNA-binding protei
50	34	100.0	532	2 T34235	hypothetical prote

ALIGNMENTS

RESULT 1

S10782  
salivary protein P-B - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C:Accession: S10782  
R:Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a  
A:Reference number: S10780; MUID:90336641  
A:Accession: S10782  
A:Molecule type: protein  
A:Residues: 1-57 <STR>  
C:Superfamily: proline-rich peptide P-B

Query Match 100.0%; Score 34; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 50 FPPPP 54

RESULT 2

PJHUSB

proline-rich peptide P-B precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 30-Nov-1979 #sequence\_revision 03-Aug-1995 #text\_change 21-Jul-2000

C:Accession: JX0321; A03297; S19281; JC7215

R:Isemura, S.; Saitoh, E.

J. Biochem. 115, 1101-1106, 1994

A:Title: Molecular cloning and sequence analysis of cDNA coding for the precursor of

A:Reference number: JX0321; MUID:95073971

A:Accession: JX0321

A:Molecule type: mRNA

A:Residues: 1-79 <ISE>

A:Cross-references: DDBJ:D29833; NID:g6630614; PIDN:BAA06213.1; PID:g705389

R:Isemura, S.; Saitoh, E.; Sanada, K.

J. Biochem. 86, 79-86, 1979

A:Title: Isolation and amino acid sequences of proline-rich peptides of human whole s

A:Reference number: A03297; MUID:80006513

A:Accession: A03297

A:Molecule type: protein

A:Residues: 23-79 <IS2>



A:Gene: msg1  
C:Superfamily: proline-rich peptide P-B

Query Match 100.0%; Score 34; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 35 FPPPP 39

RESULT 7  
S44765  
C29E4.9 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
C:Accession: S44765

Wilson, R. Submitted to the EMBL Data Library, September 1993  
A:Description: Sequence of the C. elegans cosmid C29E4.  
A:Reference number: S44738  
A:Accession: S44765  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-181 <WILL>  
A:Cross-references: EMBL:L23651; NID:g388575; PID:g388576  
C:Genetics:  
A:Introns: 46/3; 126/2; 150/3; 163/1  
C:Superfamily: Caenorhabditis elegans C29E4.9 protein

Query Match 100.0%; Score 34; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 8 FPPPP 12

RESULT 8  
T50403  
Probable succinate dehydrogenase membrane anchor subunit precursor [imported] - fission  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jun-2000  
C:Accession: T50403  
[REDACTED] Submitted to the EMBL Data Library, January 1999  
A:Reference number: Z25067  
A:Accession: T50403  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-186 <BEC>  
A:Cross-references: EMBL:AL136535; PIDN:CAB66444.1; GSPDB:GN00067; SPDB:SPBP23A10.16  
A:Experimental source: strain 972h(-); clone p1 p23A10  
C:Genetics:  
A:Gene: SPDB:SPBP23A10.16  
A:Map position: 2

Query Match 100.0%; Score 34; DB 2; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 59 FPPPP 63

RESULT 9  
B86410

protein F3M18.20 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B86410  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: B86410  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-204 <STO>  
A:Cross-references: GB:AE005172; NID:96560756; PIDN:AAF16756.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F3M18.20  
A:Map position: 1

Query Match 100.0%; Score 34; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 198 FPPPP 202

RESULT 10  
S57330  
cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)  
N:Alternate names: antimicrobial peptide; prophenin-1  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 20-Apr-2000  
C:Accession: S57330; S68726  
R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk  
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995  
A:Title: Molecular cloning and identification of a novel porcine cathelin-like antiba  
A:Reference number: S57330; MUID:96042752  
A:Accession: S57330  
A:Molecule type: mRNA  
A:Residues: 1-212 <STR>  
A:Cross-references: GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g1006757  
R:Harwig, S.L.; Kokryakov, V.N.; Swiderrek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer,  
FEBS Lett. 362, 65-69, 1995  
A:Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcin  
A:Reference number: S68726; MUID:95212585  
A:Accession: S68726  
A:Molecule type: protein  
A:Residues: 131-209 <HAR>  
A:Experimental source: leukocytes  
C:Superfamily: cathelin; cystatin homology  
C:Keywords: antibacterial  
F:6-113/Domain: cystatin homology <CYS>

Query Match 100.0%; Score 34; DB 2; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 192 FPPPP 196

RESULT 11  
T47947

hypothetical protein F2A19.150 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
 C:Accession: T47947  
 R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z24480  
 A:Accession: T47947  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-212 <DEH>  
 A:Cross-references: EMBL:AL132962  
 A:Experimental source: cultivar Columbia; BAC clone F2A19  
 C:Genetics:  
 A:Map position: 3  
 A:Note: F2A19.150  
 C:Superfamily: RING finger homology  
 F:132-183/Domain: RING finger homology <RRN>  
 Query Match 100.0%; Score 34; DB 2; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPPP 5  
 DB 9 FPPPP 13  
 RESULT 12  
 S40463  
 prophenin (PF-2) precursor - pig  
 N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S40463; S57331; S68233  
 R:Pungertcar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk,  
 FEBS Lett. 336, 284-288, 1993  
 A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial  
 A:Reference number: S40463; MUID:94085623  
 A:Accession: S40463  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-228 <PUN>  
 A:Cross-references: EMBL:X75438; NID:g443812; PIDN:CAA53188.1; PID:g443813  
 R:Strukelj, B.; Pungertcar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk,  
 Biol. Chem. Hoppe-Seyler 376, 507-510, 1995  
 A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte  
 A:Reference number: S57330; MUID:96042752  
 Accession: S57331  
 Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-228 <STR>  
 R:Zhao, C.; Ganz, T.; Lehrer, R.I.  
 FEBS Lett. 376, 130-134, 1995  
 A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen  
 A:Reference number: S68232; MUID:96105365  
 A:Accession: S68233  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-228 <ZHA>  
 A:Cross-references: EMBL:X89202; NID:g1165148; PIDN:CAA61488.1; PID:g1165149  
 C:Genetics:  
 A:Introns: 66/3; 102/3; 126/3  
 C:Superfamily: cathelin; cystatin homology  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:22-129/Domain: cystatin homology <CYS>  
 F:30-228/Product: prophenin (PF-2) #status predicted <MAT>  
 Query Match 100.0%; Score 34; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
 DB 208 FPPPP 212  
 RESULT 13  
 T45835  
 hypothetical protein F2K15.160 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 18-Feb-2000  
 C:Accession: T45835  
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemck  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23015  
 A:Accession: T45835  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-236 <RIE>  
 A:Cross-references: EMBL:AL132956  
 A:Experimental source: cultivar Columbia; BAC clone F2K15  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 35/2; 116/1; 140/2; 175/2; 190/3  
 A:Note: F2K15.160  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F2K15.160  
 Query Match 100.0%; Score 34; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPPP 5  
 DB 219 FPPPP 223  
 RESULT 14  
 A45707  
 immediate-early RL.5 circ protein - bovine herpesvirus 1 (strain K22)  
 N:Alternate names: VZV and EBV-1 homolog  
 C:Species: bovine herpesvirus 1  
 C:Date: 24-Sep-1999 #sequence\_revision 24-Sep-1999 #text\_change 24-Sep-1999  
 C:Accession: A45707  
 R:Fraefel, C.; Wirth, U.V.; Vogt, B.; Schwyzer, M.  
 J. Virol. 67, 1328-1333, 1993  
 A:Title: Immediate-early transcription over covalently joined genome ends of bovine h  
 A:Reference number: A45707; MUID:93172350  
 A:Accession: A45707  
 A:Molecule type: DNA  
 A:Residues: 1-247 <FRA>  
 A:Cross-references: GB:Z54206; NID:g995626; PIDN:CAA90913.1; PID:g995627; GB:M96453;  
 A:Note: sequence extracted from NCBI backbone (NCBIN:125354, NCBI:P:125357)  
 A:Note: source referred to as infectious bovine rhinotracheitis virus  
 Query Match 100.0%; Score 34; DB 2; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPPP 5  
 DB 149 FPPPP 153  
 RESULT 15  
 T17312  
 hypothetical protein DKFp434H018.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17312  
 R:Ottenswaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999



A:Reference number: Z18726  
A:Accession: T17312  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-253 <OTT>  
A:Cross-references: EMBL:AL117579  
A:Experimental source: adult testis; clone DKF2p434H018  
C:Genetics:  
A:Note: DKF2p434H018.1

Query Match 100.0%; Score 34; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 34 FPPPP 38

## RESULT 16

T04375  
hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740  
C:Species: Pseudomonas sp.  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 08-Oct-1999  
C:Accession: S24375  
R:Altenschmidt, U.; Bokranz, M.; Fuchs, G.  
Eur. J. Biochem. 207, 715-722, 1992  
A:Title: Novel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the plasmid p.  
A:Reference number: S24374; MUID:92339462  
A:Accession: S24375  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-272 <ALT>  
A:Cross-references: EMBL:X66604; NID:g45865; PIDN:CAA47169.1; PID:g45867  
C:Genetics:  
A:Genome: plasmid

Query Match 100.0%; Score 34; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 157 FPPPP 161

## RESULT 17

T02559  
probable spliceosome-associated protein SAP62 homolog T26B15.16 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
C:Accession: T02559; B84735  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, R.  
submitted to the EMBL Data Library, July 1998  
A:Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.  
A:Reference number: Z14678  
A:Accession: T02559  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-275 <ROU>  
A:Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298548  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.; euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: AB4420; MUID:20083487  
A:Accession: B84735  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-275 <STO>  
A:Cross-references: GB:AF002093; NID:g3298548; PIDN:AAC25942.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: Atg32600; T26B15.16  
A:Map position: 2  
A:Introns: 51/2; 108/1; 133/3; 155/3; 180/3; 205/3

Query Match 100.0%; Score 34; DB 2; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 249 FPPPP 253

## RESULT 18

T04504  
hypothetical protein F8F16.190 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 30-Apr-1999  
C:Accession: T04504  
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hohelsel, J.; M  
submitted to the Protein Sequence Database, April 1998  
A:Reference number: Z15375  
A:Accession: T04504  
A:Molecule type: DNA  
A:Residues: 1-278 <BEV>  
A:Cross-references: EMBL:AL021633  
A:Experimental source: cultivar Columbia; BAC clone F8F16  
C:Genetics:  
A:Map position: 4  
A:Note: F8F16.190

Query Match 100.0%; Score 34; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 179 FPPPP 183

## RESULT 19

T01919  
probable Ap2 domain protein - Arabidopsis thaliana  
N:Alternate names: protein T22B4.120  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 20-Jun-2000  
C:Accession: T01919; T08193  
R:Strong, C.; Graves, T.; Duckels, G.  
submitted to the EMBL Data Library, July 1998  
A:Description: The sequence of A. thaliana F2P3.  
A:Reference number: Z14455  
A:Accession: T01919  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-287 <STR>  
A:Cross-references: EMBL:AF080120; NID:g3600045; PID:g3600050  
A:Experimental source: cultivar Columbia  
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Sch  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16098  
A:Accession: T08193  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-287 <BEV>  
A:Cross-references: EMBL:AL049876  
A:Experimental source: cultivar Columbia; BAC clone T22B4  
C:Genetics:

A:Map position: 4

A:Note: P2P3.5; T22B4.120

C:Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20

Query Match 100.0%; Score 34; DB 2; Length 287;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 142 FPPPP 146

RESULT 20

T52354

hypothetical protein B11E6.30 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000

C:Accession: T52354

C:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

mitted to the Protein Sequence Database, September 2000

A:Reference number: Z26053

A:Accession: T52354

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-289 <SCH>

A:Cross-references: EMBL:AL442043; GSPDB:GNO0116; NCSP:B11E6.30

A:Experimental source: BAC clone B11E6; strain OR74A

C:Genetics:

A:Gene: NCSP:B11E6.30

A:Map position: 6

Query Match

Best Local Similarity 100.0%; Score 34; DB 2; Length 289;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 168 FPPPP 172

RESULT 21

S33209

extensin-like protein precursor - potato

C:Species: Solanum tuberosum (potato)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jul-2000

C:Accession: JT0754; S32100; S33209

C:Down, D.P.; Bolwell, G.P.; Gatehouse, J.A.

ne 134, 229-233, 1993

A:Title: Characterisation of potato (Solanum tuberosum L.) extensins: A novel extensin-

A:Reference number: JT0754; MUID:94085782

A:Accession: JT0754

A:Molecule type: mRNA

A:Residues: 1-291 <BO2>

A:Cross-references: EMBL:Z21937; NID:g296400; PIDN:CAA79930.1; PID:g296401

C:Comment: This protein is characterised by SPFP motifs and the majority of Pro residue

C:Comment: This protein is synthesized as soluble precursor which is modified, transport

C:Superfamily: hydroxyproline-rich glycoprotein

E:1-26/Domain: signal sequence #status predicted <SIG>

F:27-291/Product: extensin-like protein #status predicted <MAT>

Query Match

Best Local Similarity 100.0%; Score 34; DB 2; Length 291;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 133 FPPPP 137

RESULT 22

A36366

enhancer-binding protein C/EBP beta - mouse

N:Alternate names: alpha1-acid glycoprotein gene enhancer-binding protein; transcript

C:Species: Mus musculus (house mouse)

C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 29-Sep-1999

C:Accession: A36366; A37279; I53038

R:Chang, C.J.; Chen, T.T.; Lei, H.Y.; Chen, D.S.; Lee, S.C.

Mol. Cell. Biol. 10, 6642-6653, 1990

A:Title: Molecular cloning of a transcription factor, AGP/EBP, that belongs to member

A:Reference number: A36366; MUID:91061773

A:Accession: A36366

A:Molecule type: mRNA

A:Residues: 1-296 <CHA>

A:Cross-references: GB:M61007; NID:g191775; PIDN:AAA37192.1; PID:g191776

R:Cao, Z.; Umek, R.M.; McKnight, S.L.

Genes Dev. 5, 1538-1552, 1991

A:Title: Regulated expression of three C/EBP isoforms during adipose conversion of 3T

A:Reference number: A37279; MUID:91357470

A:Accession: A37279

A:Molecule type: mRNA

A:Residues: 1-296 <CAO>

A:Cross-references: GB:X62600; NID:g50376; PIDN:CAA44484.1; PID:g50377

R:Chang, C.J.; Shen, B.J.; Lee, S.C.

DNA Cell Biol. 14, 529-537, 1995

A:Title: Autoregulated induction of the acute-phase response transcription factor gen

A:Reference number: I53038; MUID:95322031

A:Accession: I53038

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-11 <RES>

A:Cross-references: GB:S78572; NID:g1042100

C:Genetics:

A:Gene: agp/ebp

C:Superfamily: CCAAT/enhancer-binding protein alpha

C:Keywords: DNA binding; transcription factor

Query Match

Best Local Similarity 100.0%; Score 34; DB 2; Length 296;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 124 FPPPP 128

RESULT 23

A35914

transcription factor LAP - rat

N:Alternate names: DNA-binding protein, interleukin-6 dependent; liver-enriched trans

C:Species: Rattus norvegicus (Norway rat)

C:Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 29-Sep-1999

C:Accession: A35914; A36197; B37280; S13104

R:Descombes, P.; Chojkier, M.; Lichtsteiner, S.; Falvey, E.; Schibler, U.

Genes Dev. 4, 1541-1551, 1990

A:Title: LAP, a novel member of the C/EBP gene family, encodes a liver-enriched trans

A:Reference number: A35914; MUID:91071582

A:Accession: A35914

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-297 <DES>

A:Cross-references: EMBL:X54626; NID:g56552; PIDN:CAA38443.1; PID:g56553

R:Polli, V.; Mancini, F.P.; Cortese, R.

Cell 63, 643-653, 1990

A:Title: IL-6DBP, a nuclear protein involved in interleukin-6 signal transduction, de

A:Reference number: A36197; MUID:91029495

A:Accession: A36197

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-297 <POL>

A:Cross-references: GB:M57235; GB:X54610; NID:g204917; PIDN:AAA19669.1; PID:g204918

R:Williams, S.C.; Cantwell, C.A.; Johnson, P.F.

Genes Dev. 5, 1553-1567, 1991  
A:Title: A family of C/EBP-related proteins capable of forming covalently linked leucine  
A:Reference number: A37280; MUID:91357471  
A:Accession: B37280  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 22-297 <WIL>  
A:Cross-references: GB:M84011; NID:g203602; PIDN:AAA40972.1; PID:g472404  
R:Imagawa, M.; Osada, S.; Koyama, Y.; Suzuki, T.; Hirom, P.C.; Dicciani, M.B.; Morimura  
submitted to the EMBL Data Library, July 1991  
A:Description: SF-B (Silencer Factor B) that binds to a negative element in glutathione  
A:Reference number: S16062  
A:Accession: S16062  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 77-297 <IMA>  
A:Cross-references: EMBL:X60769; NID:g57238; PIDN:CAA43179.1; PID:g57239  
C:Genetics:  
A:Gene: LAP  
Superfamily: CCAAT/enhancer-binding protein alpha  
Keywords: DNA binding; liver; transcription regulation

Query Match 100.0%; Score 34; DB 2; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 125 FPPPP 129  
|||||

RESULT 24  
TVHUJD  
Transforming protein jun-D - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change.18-Jun-1999  
C:Accession: S10184  
R:Nomura, N.; Ide, M.; Sasamoto, S.; Matsui, M.; Date, T.; Ishizaki, R.  
Nucleic Acids Res. 18, 3047-3048, 1990  
A:Title: Isolation of human cDNA clones of jun-related genes, jun-B and jun-D.  
A:Reference number: S10183; MUID:90272414  
A:Accession: S10184  
A:Molecule type: mRNA  
A:Residues: 1-303 <NOM>  
A:Cross-references: EMBL:X51346; NID:g34016; PIDN:CAA35739.1; PID:g34017  
C:Genetics:  
A:Gene: GDB:JUND  
Cross-references: GDB:125380; OMIM:165162  
Map position: 19p13.1-19p13.1  
C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology  
C:Keywords: DNA binding; leucine zipper; proto-oncogene; transcription regulation; trans  
F:219-259/Domain: fos/jun DNA-binding domain homology <FJD>  
F:252-280/Region: leucine zipper motif

Query Match 100.0%; Score 34; DB 1; Length 303;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 178 FPPPP 182  
|||||

RESULT 25  
C84635  
hypothetical protein At2g24320 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: C84635  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

Query Match 100.0%; Score 34; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 15 FPPPP 19  
|||||

Search completed: July 7, 2002, 10:13:28  
Job time: 90 sec

uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: C84635  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-316 <STO>  
A:Cross-references: GB:AE002093; NID:g4337191; PIDN:AA18105.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g24320  
A:Map position: 2

Query Match 100.0%; Score 34; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 15 FPPPP 19  
|||||



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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:13:33 ; Search time 12.61 Seconds  
(without alignments)  
15.353 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	57	1 PRPB_HUMAN	P02814 homo sapien
2	34	100.0	181	1 YK69_CAEEL	P34347 caenorhabdi
3	34	100.0	212	1 PF11_PIG	P51524 sus scrofa
4	34	100.0	228	1 PF12_PIG	P51525 sus scrofa
5	34	100.0	288	1 FXE3_MOUSE	Q9qy14 mus musculu
6	34	100.0	292	1 SHOX_HUMAN	O15266 homo sapien
7	34	100.0	296	1 CEBB_MOUSE	P28033 mus musculu
8	34	100.0	322	1 UL15_HCMVA	P21272 rattus norv
9	34	100.0	322	1 CEBB_MOUSE	P16844 human cytom
10	34	100.0	341	1 JUND_MOUSE	P15066 mus musculu
11	34	100.0	341	1 JUND_MOUSE	P52909 rattus norv
12	34	100.0	347	1 JUND_MOUSE	P17535 homo sapien
13	34	100.0	391	1 RBM9_HUMAN	O43251 homo sapien
14	34	100.0	456	1 FXD1_MOUSE	Q61345 mus musculu
15	34	100.0	468	1 YL34_CAEEL	P34425 caenorhabdi
16	34	100.0	491	1 PRCC_HUMAN	Q92733 homo sapien
17	34	100.0	493	1 NPXR_MOUSE	Q99185 mus musculu
18	34	100.0	494	1 NPXR_MOUSE	O35764 rattus norv
19	34	100.0	542	1 ZYX_CHICK	Q04584 gallus gall
20	34	100.0	564	1 ZYX_MOUSE	Q62523 mus musculu
21	34	100.0	572	1 ZYX_HUMAN	Q15942 homo sapien
22	34	100.0	584	1 YBX1_SCHPO	Q10207 schizosacch
23	34	100.0	639	1 ACTA_LISMO	P33379 listeria mo
24	34	100.0	653	1 SCBL_MOUSE	Q9eqg3 mus musculu
25	34	100.0	668	1 SCBL_HUMAN	O95171 homo sapien
26	34	100.0	774	1 AD28_MOUSE	Q9jln6 mus musculu
27	34	100.0	783	1 FYB_HUMAN	O15117 homo sapien
28	34	100.0	804	1 MEA6_HUMAN	O15320 homo sapien
29	34	100.0	819	1 FYB_MOUSE	O35601 mus musculu
30	34	100.0	825	1 SE5_RAT	Q63003 rattus norv
31	34	100.0	848	1 YBV8_YEAST	P38266 saccharomyc
32	34	100.0	992	1 EBN6_EBV	P03204 epstein-bar
33	34	100.0	1024	1 SREL_RAT	P56720 rattus norv

34	34	100.0	1065	1 VINC_CHICK	P12003 gallus gall
35	34	100.0	1065	1 VINC_HUMAN	P18206 homo sapien
36	34	100.0	1065	1 VINC_MOUSE	Q64727 mus musculu
37	34	100.0	1069	1 C910_HUMAN	Q9n2b2 homo sapien
38	34	100.0	1111	1 GLI1_MOUSE	P47806 mus musculu
39	34	100.0	1133	1 SREL_CRIGR	Q60416 cricetus
40	34	100.0	1164	1 FHOS_HUMAN	Q9y613 homo sapien
41	34	100.0	1196	1 ABL1_CAEEL	P03949 caenorhabdi
42	34	100.0	1217	1 AF4_MOUSE	O88573 mus musculu
43	34	100.0	1250	1 SSD1_YEAST	P24276 saccharomyc
44	34	100.0	1520	1 ABL_DROME	P00522 drosophila
45	34	100.0	1528	1 KEM1_YEAST	P22147 saccharomyc
46	34	100.0	1841	1 CC12_SCHPO	Q10059 schizosacch
47	34	100.0	1874	1 POLR_KIMVJ	P36304 kennedy ye
48	34	100.0	1882	1 POL2_TRSVJ	P25247 tomato ring
49	34	100.0	3511	1 MY15_MOUSE	Q9qz24 mus musculu
50	34	100.0	4590	1 FATH_HUMAN	Q14517 homo sapien

## ALIGNMENTS

RESULT 1  
PRPB\_HUMAN STANDARD; PRT; 57 AA.  
AC P02814;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Proline-rich peptide P-B [Contains: Peptide P-A].  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Saliva;  
RX MEDLINE=80006513; PubMed=479131;  
RA Isemura S., Saitoh E., Sanada K.;  
RT "Isolation and amino acid sequences of proline-rich peptides of human whole saliva.";  
RL J. Biochem. 86:79-86(1979).  
CC -!- PTM: P-A IS PROBABLY A DEGRADATION PRODUCT OF P-B.  
DR PIR: A03297; PJHUSB.  
KW Repeat; Saliva.  
FT CHAIN 1 57 PROLINE-RICH PEPTIDE P-B.  
FT CHAIN 20 57 PEPTIDE P-A.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 57 AA; 5810 MW; 2085FBB83BAFD063 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
DB 50 FPPPP 54

RESULT 2  
YK69\_CAEEL STANDARD; PRT; 181 AA.  
AC P34347;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Hypothetical 20.1 kDa protein C29E4.9 in chromosome III.  
GN C29E4.9.

OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;

```

[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN-BRISTOL N2;
RX  MEDLINE=94150718; PubMed=7906398;
RA  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA  Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA  Craton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA  Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA  Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA  Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA  Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA  Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA  Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA  Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA  Wohlman P.;
RA  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans.";
RL  Nature 368:32-38(1994).
-----
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-----
CC  EMBL; L23651; AAA27956.1; -.
DR  PIR; S44765; S44765.
DR  WormPep; C29E4.9; CE00091.
KW  Hypothetical protein.
SQ  SEQUENCE 181 AA; 20132 MW; 85CEFB161F40BB4A CRC64;

Query Match      100.0%; Score 34; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FPPPPP 5
DB  8 FPPPPP 12

RESULT 3
PF11_PIG
ID  PF11_PIG      STANDARD;      PRT; 212 AA.
AC  P51524;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Prophenin-1 precursor (PF-1) (C6) (Fragment).
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Bone marrow;
RX  MEDLINE=96042752; PubMed=7576250;
RA  Strukelj B., Pungercar J., Kopitar G., Renko M., Lenarcic B.,
RA  Berbic S., Turk V.;
RT  "Molecular cloning and identification of a novel porcine
RT  cathelin-like antibacterial peptide precursor.";
RL  Biol. Chem. Hoppe-Seyler 376:507-510(1995).
RN  [2]
RP  SEQUENCE OF 131-209.
RC  TISSUE=Blood;
RX  MEDLINE=95212585; PubMed=7598355;
RA  Harwig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M.,
RA  Zhao C., Lehrer R.I.;
RT  "Prophenin-1, an exceptionally proline-rich antimicrobial peptide
RT  from porcine leukocytes.";
RL  FEBS Lett. 362:65-69(1995).
```

```

CC  -!- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE
CC  AGAINST GRAM-NEGATIVE BACTERIA THAN GRAM-POSITIVE BACTERIA.
CC  -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
-----
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-----
CC  EMBL; X86031; CAA60023.1; -.
DR  InterPro; IPR001894; Cathelicidin.
DR  Pfam; PF00666; Cathelicidins; 1.
DR  ProDom; PD001838; Cathelicidins; 1.
DR  PROSITE; PS00946; CATHELICIDINS_1; 1.
DR  PROSITE; PS00947; CATHELICIDINS_2; 1.
KW  Antibiotic; Repeat; Amidation; Signal.
FT  SIGNAL      <1 13      POTENTIAL.
FT  PROPEP      14 130     POTENTIAL.
FT  PEPTIDE     131 209    PROPENIN-1.
FT  PROPEP      210 212    REMOVED IN NATURE FORM (POTENTIAL).
FT  MOD_RES     14 14      PYRROLIDONE CARBOXYLIC ACID (BY
FT                                     SIMILARITY).
FT  DISULFID     69 80      BY SIMILARITY.
FT  DISULFID     91 108     BY SIMILARITY.
FT  MOD_RES      209 209    AMIDATION (G-210 PROVIDE AMIDE GROUP)
FT                                     (POTENTIAL).
FT  DOMAIN      116 212     PRO-RICH.
FT  DOMAIN      132 201     7 X 10 AA TANDEM REPEATS.
FT  REPEAT      132 141     1.
FT  REPEAT      142 151     2.
FT  REPEAT      152 161     3.
FT  REPEAT      162 171     4.
FT  REPEAT      172 181     5.
FT  REPEAT      182 191     6.
FT  REPEAT      192 201     7.
SQ  SEQUENCE 212 AA; 23956 MW; A315414C90DBF423 CRC64;

Query Match      100.0%; Score 34; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FPPPPP 5
DB  192 FPPPPP 196

RESULT 4
PF12_PIG
ID  PF12_PIG      STANDARD;      PRT; 228 AA.
AC  P51525;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Prophenin-2 precursor (PF-2) (C12) (Prophenin-1 like).
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Bone marrow;
RX  MEDLINE=94085623; PubMed=8262247;
RA  Pungercar J., Strukelj B., Kopitar G., Renko M., Lenarcic B.,
RA  Gusensek F., Turk V.;
RT  "Molecular cloning of a putative homolog of proline/arginine-rich
RT  antibacterial peptides from porcine bone marrow.";
RL  FEBS Lett. 336:284-288(1993).
RN  [2]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RL peptides: prophenin-2 and PR-39.";
RL FEBS Lett. 376:130-134(1995).
CC -!- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE
CC AGAINST GRAM-NEGATIVE BACTERIA THAN GRAM-POSITIVE BACTERIA.
CC -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC -----
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CC -----
CC EMBL; X75438; CAA53188.1; -.
CC EMBL; X89202; CAA61488.1; -.
CC InterPro; IPR001894; Cathelicidin.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidins; 1.
CC DR PROSITE; PS00946; CATHELICIDINS 1; 1.
CC DR PROSITE; PS00947; CATHELICIDINS 2; 1.
CC KW Antibiotic; Repeat; Amidation; Signal.
CC FT SIGNAL 1 29
CC FT PROPEP 30 146
CC FT PEPTIDE 147 225
CC FT PROPEP 226 228
CC FT .MOD_RES 225 225
CC FT DOMAIN 132 228
CC FT DOMAIN 148 217
CC FT REPEAT 148 157
CC FT REPEAT 158 167
CC FT REPEAT 168 177
CC FT REPEAT 178 187
CC FT REPEAT 188 197
CC FT REPEAT 198 207
CC FT REPEAT 208 217
CC FT MOD_RES 30 30
CC FT PYRROLIDONE CARBOXYLIC ACID (BY
CC FT DISULFID 85 96
CC FT DISULFID 107 124
CC FT BY SIMILARITY.
CC SEQUENCE 228 AA; 25855 MW; 1EA4511FF35CC182 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 208 FPPPP 212

RESULT 5
FXE3_MOUSE STANDARD; PRT; 288 AA.
AC Q9Y14;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein E3.
GN FOXE3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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```
RC STRAIN=129/SV; TISSUE=Lens;
RX MEDLINE=20119184; PubMed=10652278;
RA Blixt A., Mahlapuu M., Altola M., Peltto-Huikko M., Enerback S.,
RA Carlsson P.;
RT "A forkhead gene, Foxe3, is essential for lens epithelial
RT proliferation and closure of the lens vesicle.";
RL Genes Dev. 14:245-254(2000).
CC -!- FUNCTION: TRANSCRIPTION FACTOR ESSENTIAL FOR LENS EPITHELIAL
CC PROLIFERATION AND CLOSURE OF THE LENS VESICLE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LENS FROM THE
CC START OF LENS PLACODE INDUCTION AND BECOMES RESTRICTED TO THE
CC ANTERIOR PROLIFERATING CELLS WHEN LENS FIBER DIFFERENTIATION
CC BEGINS.
CC -!- DISEASE: DEFECTS IN FOXE3 ARE A CAUSE OF DYSGENETIC LENS (DYL); IN
CC MOUSE MUTANT DYL THE LENS VESICLE FAILS TO SEPARATE FROM THE
CC ECTODERM, CAUSING A FUSION BETWEEN THE LENS AND THE CORNEA. LACK
CC OF A PROLIFERATING ANTERIOR LENS EPITHELIUM LEADS TO ABSENCE OF
CC SECONDARY LENS FIBERS AND A DYSPLASTIC, CATARACTIC LENS.
CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC -----
CC EMBL; AF142647; AAF15997.1; -.
CC HSSP; O63245; 2HFH.
CC MGD; MGI:1353569; Foxe3.
CC InterPro; IPR001766; Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC SMART; SM00339; FH; 1.
CC DR PROSITE; PS00657; FORK_HEAD_1; 1.
CC DR PROSITE; PS00658; FORK_HEAD_2; 1.
CC DR PROSITE; PS50039; FORK_HEAD_3; 1.
CC KW Transcription regulation; DNA-binding; Nuclear protein.
CC FT DOMAIN 55 58
CC FT DNA_BIND 63 154
CC FT DOMAIN 166 176
CC FT DOMAIN 179 186
CC FT DOMAIN 229 232
CC FT POLY-ALA.
CC SEQUENCE 288 AA; 30541 MW; 16425926F3E466C5 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 180 FPPPP 184

RESULT 6
SHOX_HUMAN STANDARD; PRT; 292 AA.
AC O15266; O15267; O00412; O00413;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Short stature homeobox protein (Short stature homeobox containing
DE protein) (Pseudoautosomal homeobox containing osteogenic protein).
GN (SHOX) OR PHOGX OR SHOX OR PHOG) AND (SHOXY OR PHOXY OR PHOG).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SHOXA AND SHOXB).
```





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CC -----
DR EMBL; X62600; CAA44484.1; -.
DR EMBL; M61007; AAA37192.1; -.
DR EMBL; S78572; -. NOT_ANNOTATED_CDS.
DR PIR; A37279; A37279.
DR PIR; A36366; A36366.
DR TRANSFAC; T00017; -.
DR MGD; MGI:88373; Cebpb.
DR InterPro; IPR001871; bZIP.
DR Pfam; PF00170; bZIP; 1.
DR SMART; SM00338; BRLZ; 1.
DR Transcription regulation; Activator; DNA-binding; Nuclear protein;
KW Trans-acting factor
FT DOMAIN 120 129
FT PRO-RICH.
FT DOMAIN 170 191
FT PRO/SER-RICH.
FT DNA_BIND 228 244
FT BASIC MOTIF.
FT DOMAIN 257 285
FT LEUCINE-ZIPPER.
FT SEQUENCE 296 AA; 31445 MW; 827AC4AFC209AE89 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 124 FPPPP 128

RESULT 8
CEBB_RAT
ID CEBB_RAT STANDARD; PRT; 297 AA.
AC P21272;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CCAT/enhancer binding protein beta (C/EBP beta) (Interleukin-6-
DE dependent binding protein) (IL-6DBP) (Liver-enriched transcriptional
DE activator) (LAP) (Silencer factor B) (SF-B) (C/EBP-related protein 2).
GN CEBPB OR SPB OR CRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=91029495; PubMed=2171780;
Poli V., Mancini F.P., Cortese R.;
"IL-6DBP, a nuclear protein involved in interleukin-6 signal
transduction, defines a new family of leucine zipper proteins related
to C/EBP.";
Cell 63:643-653(1990).
RN [2]
SEQUENCE FROM N.A.
STRAIN-LEWIS; TISSUE=Liver;
MEDLINE=91071582; PubMed=2253878;
Descombes P., Chojkier M., Lichtsteiner S., Falvey E., Schibler U.;
"LAP, a novel member of the C/EBP gene family, encodes a
liver-enriched transcriptional activator protein.";
Genes Dev. 4:1541-1551(1990).
RN [3]
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
MEDLINE=92319638; PubMed=1377818;
Thomassin H., Hamel D., Bernier D., Guertin M., Belanger L.;
"Molecular cloning of two C/EBP-related proteins that bind to the
promoter and the enhancer of the alpha 1-fetoprotein gene. Further
analysis of C/EBP beta and C/EBP gamma.";
Nucleic Acids Res. 20:3091-3098(1992).
RN [4]
SEQUENCE OF 77-297 FROM N.A.
```

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RC TISSUE=Liver;
RA Imagawa M., Osada S., Koyama Y., Suzuki T., Hirom P.C.,
RA Diccianni M.B., Morimura S., Muramatsu M.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RL [5]
RP SEQUENCE OF 22-297 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver, Adipose tissue, and Lung;
RX MEDLINE=91357471; PubMed=1884998;
RA Williams S.C., Cantwell C.A., Johnson P.F.;
RT "A family of C/EBP-related proteins capable of forming covalently
RT linked leucine zipper dimers in vitro.";
RL Genes Dev. 5:1553-1567(1991).
CC -!- FUNCTION: INVOLVED IN INTERLEUKIN-6 SIGNAL TRANSDUCTION,
CC INCLUDING THE TRANSCRIPTIONAL ACTIVATION OF ACUTE-PHASE GENES.
CC -!- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMERS
CC WITH C/EBP ALPHA AND GAMMA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: LIVER AND LUNG.
CC -!- SIMILARITY: TO OTHER BZIP PROTEINS. STRONG, TO OTHER C/EBP
CC PROTEINS.
CC -----
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CC -----
DR EMBL; M57235; AAA19669.1; -.
DR EMBL; X54626; CAA38443.1; -.
DR EMBL; X60769; CAA43179.1; -.
DR EMBL; M84011; AAA40972.1; -.
DR PIR; A36197; A36197.
DR PIR; A35914; A35914.
DR TRANSFAC; T00459; -.
DR InterPro; IPR001871; bZIP.
DR Pfam; PF00170; bZIP; 1.
DR SMART; SM00338; BRLZ; 1.
KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
KW Trans-acting factor.
FT DOMAIN 121 130
FT PRO-RICH.
FT DOMAIN 171 192
FT PRO/SER-RICH.
FT DNA_BIND 229 245
FT BASIC MOTIF.
FT DOMAIN 258 286
FT LEUCINE-ZIPPER.
FT SEQUENCE 297 AA; 31502 MW; C2511FDB6527789 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 125 FPPPP 129

RESULT 9
UL15_HCMVA
ID UL15_HCMVA STANDARD; PRT; 322 AA.
AC P16844;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Hypothetical protein UL15.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=90269039; PubMed=2161319;
```

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RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,  
RA Horneil T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,  
RA Freddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.,  
RT "Analysis of the protein-coding content of the sequence of human  
RL cytomegalovirus strain Ad169."  
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).  
CC -----  
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CC -----  
DR EMBL; X17403; CA35415.1; -  
DR PIR; S09779; S09779.  
KW Hypothetical protein.  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 322 AA; 35337 MW; CB3DE38895E3A0E8 CRC64;  
-----  
Query Match 100.0%; Score 34; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 267 FPPPP 271  
-----  
RESULT 10  
JUND_MOUSE STANDARD; PRT; 341 AA.  
ID JUND_MOUSE  
AC P15056;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Transcription factor jun-D.  
GN JUND OR JUND1 OR JUN-D.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=89160806; PubMed=2493644;  
RA Ryder K., Lanahan A., Perez-Albuerne E., Nathans D.,  
RT "jun-D: a third member of the jun gene family."  
Proc. Natl. Acad. Sci. U.S.A. 86:1500-1503(1989).  
[2]  
SEQUENCE FROM N.A.  
RX MEDLINE=89356612; PubMed=2504580;  
RA Hirai S.I., Ryseck R.P., Mehta F., Bravo R., Yaniv M.,  
RT "Characterization of junb: a new member of the jun proto-oncogene  
family."  
EMBO J. 8:1433-1439(1989).  
[3]  
SEQUENCE FROM N.A.  
RX MEDLINE=90110219; PubMed=2104845;  
RA Li L., Hu J.-S., Olson E.N.;  
RT "Different members of the jun proto-oncogene family exhibit distinct  
RT patterns of expression in response to type beta transforming growth  
RT factor."  
J. Biol. Chem. 265:1556-1562(1990).  
CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: BRAIN AND KIDNEY.  
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.  
-----  
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CC -----  
DR EMBL; J04509; AAA39344.1; -  
DR EMBL; X15358; CAA33418.1; -  
DR EMBL; J05205; AAA39345.1; -  
DR PIR; A32158; TVMSJD.  
DR PIR; A35013; A35013.  
DR HSSP; P05412; IFOS.  
DR TRANSFAC; T00437; -  
DR MGD; MGI:96648; Jund1.  
DR InterPro; IPR002112; Leuzip_Jun.  
DR InterPro; IPR001871; bZIP.  
DR Pfam; PF00170; bZIP; 1  
DR PRINTS; PR00043; LEUZIPRJUN.  
DR SMART; SM00338; BRLZ; 1.  
DR PROSITE; PS00036; bZIP_BASIC; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DNA_BIND 268 286 BASIC MOTIF.  
FT DOMAIN 290 318 LEUCINE-ZIPPER.  
FT CONFLICT 5 5 F -> L (IN REF. 3).  
FT CONFLICT 61 62 EQ -> DE (IN REF. 3).  
FT CONFLICT 317 318 QL -> HV (IN REF. 3).  
SQ SEQUENCE 341 AA; 34904 MW; 2727392F6B65188D CRC64;  
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Query Match 100.0%; Score 34; DB 1; Length 341;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 212 FPPPP 216  
-----  
RESULT 11  
JUND_RAT STANDARD; PRT; 341 AA.  
ID JUND_RAT  
AC P52909;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Transcription factor jun-D.  
GN JUND OR JUN-D.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;  
RX MEDLINE=95180737; PubMed=7875605;  
RA Yamada T., Nakao S., Osada S., Imagawa M., Nishihara T.,  
RT "Sequence analysis of the rat jun-D gene."  
Gene 153:285-286(1995).  
CC -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.  
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CC -----  
DR EMBL; D26307; BAA05369.1; -  
DR HSSP; P05412; IFOS.  
DR TRANSFAC; T02197; -  
DR InterPro; IPR002112; Leuzip_Jun.
```

DR InterPro; IPR001871; bZIP.  
DR Pfam; PF00170; bZIP; 1.  
DR PRINTS; PR00043; LEUZIPPRJUN.  
DR SMART; SM00338; BRLZ; 1.  
DR PROSITE; PS00036; BZIP\_BASIC; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DNA\_BIND 268 286 BASIC MOTIF.  
FT DOMAIN 290 318 LEUCINE-ZIPPER.  
SQ SEQUENCE 341 AA; 34874 MW; 2D9BF92313101988 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 341;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 212 FPPPP 216

## JULT 12

RM9\_HUMAN  
ID JUND\_HUMAN STANDARD; PRT; 347 AA.  
AC P17535;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Transcription factor jun-D.  
GN JUND.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91232849; PubMed=1903194;  
RA Berger I., Shaul Y.;  
RT "Structure and function of human jun-D.";  
RL Oncogene 6:561-566(1991).  
RN [2]  
RP SEQUENCE OF 45-347 FROM N.A.  
RX MEDLINE=90272414; PubMed=2112242;  
RA Nomura N., Ide M., Sasamoto S., Matsui M., Date T., Ishizaki R.;  
RT "Isolation of human cDNA clones of jun-related genes, jun-B and jun-D.";  
RL Nucleic Acids Res. 18:3047-3048(1990).  
CC -!- FUNCTION: BINDS AN AP-1 SITE AND UPON COTRANSFECTION STIMULATES THE ACTIVITY OF A PROMOTER THAT BEARS AN AP-1 SITE.  
CC -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.  
CC -----  
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CC -----

DR EMBL; X56681; CAA40010.1; -  
DR EMBL; X51346; CAA35739.1; -  
DR PIR; S10184; TVHJUD.  
DR PIR; A43815; A43815.  
DR HSP; P05412; IFOS.  
DR TRANSFAC; T01978; -  
DR MIM; 165162; -  
DR InterPro; IPR002112; Leuzip\_Jun.  
DR InterPro; IPR001871; bZIP.  
DR PRINTS; PR00170; bZIP; 1.  
DR PRINTS; PR00043; LEUZIPPRJUN.  
DR SMART; SM00338; BRLZ; 1.  
DR PROSITE; PS00036; BZIP\_BASIC; 1.

KW Transcription regulation; DNA-binding; Activator; Nuclear protein.  
FT DOMAIN 158 166 POLY-ALA.  
FT DNA\_BIND 273 292 BASIC MOTIF.  
FT DOMAIN 296 324 LEUCINE-ZIPPER.  
FT CONFLICT 66 66 P -> A (IN REF. 2).  
FT CONFLICT 69 71 ASY -> PPT (IN REF. 2).  
FT CONFLICT 73 74 PA -> LR (IN REF. 2).  
FT CONFLICT 157 157 R -> A (IN REF. 2).  
SQ SEQUENCE 347 AA; 35224 MW; 04A91A87C296F5BD CRC64;

Query Match 100.0%; Score 34; DB 1; Length 347;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 222 FPPPP 226

## RESULT 13

RM9\_HUMAN  
ID RBM9\_HUMAN STANDARD; PRT; 391 AA.  
AC O43251; Q9UGW4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Putative RNA-binding protein 9 (RNA binding motif protein 9).  
GN RBM9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Placenta;  
RA Collins J.E., Burton J.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 86-391 FROM N.A.  
RA Whiteley M.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).  
CC -----  
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CC -----

DR EMBL; AL009266; CAA15842.1; ALT\_SEQ.  
DR EMBL; AL049748; CAB63054.1; -  
DR HSP; P09012; ZUJA.  
DR InterPro; IPR000504; RRM.  
DR Pfam; PF00076; rrm; 1.  
DR SMART; SM00360; RRM; 1.  
DR PROSITE; PS50102; RRM; 1.  
DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
KW RNA-binding.  
FT DOMAIN 112 188 RNA-BINDING (RRM).  
SQ SEQUENCE 391 AA; 42284 MW; ED2B76C023D16A7B CRC64;

Query Match 100.0%; Score 34; DB 1; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
|||||  
Db 30 FPPPP 34

```
RESULT 14
FXDI_MOUSE
ID FXDI_MOUSE STANDARD; PRT; 456 AA.
AC Q61345;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-
DE related transcription factor 4) (FREAC-4).
GN FOXD1 OR FKHL8 OR FREAC4 OR HFHBF2.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Embryo;
RX MEDLINE=95114592; PubMed=7815060;
RA Hatini V., Tao W., Lai E.;
RA "Expression of winged helix genes, BF-1 and BF-2, define adjacent
RA domains within the developing forebrain and retina.";
RA J. Neurobiol. 25:1293-1309(1994).
CC -!- FUNCTION: MAY FUNCTION IN SPECIFYING POSITIONAL IDENTITY IN THE
CC DEVELOPING RETINA AS WELL AS THE SUBDIVISION OF THE FOREBRAIN
CC NEUROEPITHELIUM.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE CNS AND
CC TEMPORAL HALF OF THE RETINA. ALSO EXPRESSED IN THE CONDENSED HEAD
CC MESENCHYME, METANEPHRIC BLASTOMA OF THE DEVELOPING KIDNEY, CORTEX
CC OF THE ADRENAL GLAND, CONDENSED MESENCHYME AT THE BASE OF THE
CC FOLLICLES OF VIBRASAE, AND CARTILAGE PERICHONDRUM OF THE
CC DEVELOPING VERTEBRATE.
CC -!- DEVELOPMENTAL STAGE: AT E9.5 EMBRYOS, EXPRESSED IN A LIMITED
CC REGION OF THE NEUROEPITHELIUM AND ALSO IN THE TEMPORAL HALF OF THE
CC PRIMARY OPTIC CUP AND THE OPTIC STALK. AT E10.5, SEEN IN THE
CC HYPOTHALAMUS, TEMPORAL HALF OF THE OPTIC STALK, AND TEMPORAL
CC HEMIRETINA. AT E12.5 AND E13.5 A HIGH EXPRESSION IS SEEN IN
CC REGIONS OF CONDENSED MESENCHYME OF THE HEAD, AND AS
CC NEUROEPITHELIAL CELLS BEGIN TO DIFFERENTIATE AND MIGRATE OUTWARD
CC FROM THE VENTRICULAR ZONE, EXPRESSION DECLINES MARKEDLY. BY E16.5
CC LEVELS ARE DIMINISHED AND RESTRICTED TO UNFUSED POCKETS ALONG THE
CC EXHAUSTED VENTRICULAR ZONE.
CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -!- CAUTION: WAS ORIGINALLY (REF.1) ASSIGNED TO BE BF-2 (FOXG1A).
CC -----
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CC -----
CC EMBL; L38607; AAC42042.1;
CC HSSP; Q63245; 2HFH.
CC TRANSFAC; T02293;
CC MGD; MGI:1347463; Foxd1.
CC InterPro; IPR001766; Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC SMART; SM00339; FH; 1.
CC PROSITE; PS00657; FORK_HEAD_1; 1.
CC PROSITE; PS00658; FORK_HEAD_2; 1.
CC PROSITE; PS50039; FORK_HEAD_3; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC Developmental protein.
FT DOMAIN 29 32 POLY-GLU.
FT DOMAIN 33 36 POLY-ASP.
FT DOMAIN 38 46 POLY-GLY.
FT DOMAIN 55 58 POLY-ARG.
FT DOMAIN 73 76 POLY-ASP.
FT DNA_BIND 130 224
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FT DOMAIN 261 267 POLY-PRO.
FT DOMAIN 293 302 POLY-ALA.
FT DOMAIN 308 319 POLY-PRO.
FT DOMAIN 395 400 POLY-GLY.
FT DOMAIN 420 425 POLY-ALA.
SQ SEQUENCE 456 AA; 45429 MW; 43D93F89BDBFCC7 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 260 FPPPP 264

RESULT 15
YL34_CAEEL STANDARD; PRT; 468 AA.
AC P34425;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 53.6 kDa protein F44B9.4 in chromosome III.
GN F44B9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Cullton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RA elegans.";
RA Nature 368:32-38(1994).
CC -----
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CC -----
CC EMBL; L23648; AAA28034.1;
CC PIR; S44815; S44815.
CC WormPep; F44B9.4; CE00551.
CC InterPro; IPR000553; Cyclin.
CC Pfam; PF00134; cyclin; 1.
CC SMART; SM00385; CYCLIN; 1.
CC KW Hypothetical protein.
SQ SEQUENCE 468 AA; 53569 MW; 9E0C2B41A050A256 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 260 FPPPP 264
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Db 397 FPPPP 401

RESULT 16
PRCC_HUMAN STANDARD; PRT; 491 AA.
AC Q92733; O00724; O00665;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Proline-rich protein PRCC.
GN PRCC OR TPRC
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA "Mouse neuronal pentraxin receptor."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF316612; AAK11300.1; -.
DR EMBL; AF318076; AAK06717.1; -.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR PRODOM; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS IN FETAL AND ADULT TISSUES.
CC -!- DISEASE: INVOLVED IN PAPILLARY RENAL CELL CARCINOMA (PRCC) BY
CC A CHROMOSOMAL TRANSLOCATION T(X;1)(P11.2;Q21.2) WHICH INVOLVES
CC TFE3 AND PRCC.
CC -----
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CC -----
EMBL; X97124; CAA65791.1; -.
EMBL; X99720; CAA68060.1; -.
MIM; 179755; -.
KW Chromosomal translocation; Proto-oncogene.
FT DOMAIN 18 25 POLY-GLU.
FT DOMAIN 52 55 POLY-PRO.
FT DOMAIN 79 84 POLY-PRO.
FT DOMAIN 91 94 POLY-PRO.
FT DOMAIN 235 239 POLY-THR.
SQ SEQUENCE 491 AA; 52417 MW; F99CFD9D42725D57 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 90 FPPPP 94

RESULT 17
NPXR_MOUSE STANDARD; PRT; 493 AA.
AC Q99J85;
DT 16-OCT-2001 (Rel. 40, Created)

Query Match 100.0%; Score 34; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 90 FPPPP 94
```

```
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuronal pentraxin receptor.
GN NPTRX OR NPR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RC Perin M.S.;
RT "Mouse neuronal pentraxin receptor."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF316612; AAK11300.1; -.
DR EMBL; AF318076; AAK06717.1; -.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR PRODOM; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
DR PROSITE; PS00289; PENTAXIN; 1.
KW Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS IN FETAL AND ADULT TISSUES.
CC -!- DISEASE: INVOLVED IN PAPILLARY RENAL CELL CARCINOMA (PRCC) BY
CC A CHROMOSOMAL TRANSLOCATION T(X;1)(P11.2;Q21.2) WHICH INVOLVES
CC TFE3 AND PRCC.
CC -----
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CC -----
EMBL; X97124; CAA65791.1; -.
EMBL; X99720; CAA68060.1; -.
MIM; 179755; -.
KW Chromosomal translocation; Proto-oncogene.
FT DOMAIN 18 25 POLY-GLU.
FT DOMAIN 52 55 POLY-PRO.
FT DOMAIN 79 84 POLY-PRO.
FT DOMAIN 91 94 POLY-PRO.
FT DOMAIN 235 239 POLY-THR.
SQ SEQUENCE 491 AA; 52417 MW; F99CFD9D42725D57 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 82 FPPPP 86

RESULT 18
NPXR_RAT STANDARD; PRT; 494 AA.
AC O35764;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuronal pentraxin receptor.
GN NPTRX OR NPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97407943; PubMed=9261167;
RA Dodds D.C., Omeis I.A., Cushman S.J., Helms J.A., Perin M.S.;
RT "Neuronal pentraxin receptor, a novel putative integral membrane
```

RT pentraxin that interacts with neuronal pentraxin 1 and 2 and  
RL J. Biol. Chem. 272:21488-21494(1997).  
CC -!- SUBUNIT: BINDS TO NPTX1, NPTX2 AND TAPOXIN-ASSOCIATED CALCIUM-  
CC BINDING PROTEIN 49 (TCBP49).  
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).  
CC -!- TISSUE SPECIFICITY: Brain-specific.  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
CC  
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CC  
CC EMBL; AF005099; AAB62885.1; -  
DR HSP; P02743; ISAC.  
DR InterPro: IPR001759; Pentaxin.  
DR Pfam: PF00354; pentaxin.1.  
DR PRINTS; PR00895; PENTAXIN.  
DR ProDom; PD002153; Pentaxin; 1.  
DR SMART; SM00159; PTX; 1.  
DR PROSITE; PS00289; PENTAXIN; FALSE NEG.  
KW Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor.  
FT DOMAIN 1 2 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 3 23 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
(POTENTIAL).  
FT DOMAIN 24 494 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 290 494 PENTAXIN.  
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 494 AA; 52370 MW; FEC996CA311E40E2 CRC64;  
SQ  
  
Query Match 100.0%; Score 34; DB 1; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
Db 82 FPPPP 86  
|||||  
  
RESULT 19  
ZYX\_CHICK STANDARD; PRT; 542 AA.  
Q04584;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zyxin.  
GN ZYX.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93107157; PubMed=1469049;  
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;  
RT "Zyxin and CRP: two interactive LIM domain proteins associated with  
the cytoskeleton.";  
RL J. Cell Biol. 119:1573-1587(1992).  
CC -!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP  
PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT  
MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN  
CYTOSKELETON NEAR THE ADHESION PLAQUES.  
CC

CC -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2  
ZINC IONS.  
CC  
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CC  
CC EMBL; X69190; CAA48936.1; -  
DR PIR; A44358; A44358.  
DR InterPro: IPR001781; LIM.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam: PF00412; LIM; 3.  
DR ProDom; PD000094; LIM; 3.  
DR SMART; SM00132; LIM; 3.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
DR PROSITE; PS00023; LIM\_DOMAIN\_2; 3.  
KW Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.  
FT DOMAIN 83 90 PRO-RICH.  
FT DOMAIN 103 130 PRO-RICH.  
FT DOMAIN 352 411 LIM 1.  
FT DOMAIN 412 471 LIM 2.  
FT DOMAIN 472 538 LIM 3.  
FT VARIANT 463 463 D -> V.  
FT SEQUENCE 542 AA; 58537 MW; 9D898AC180C680FC CRC64;  
SQ  
  
Query Match 100.0%; Score 34; DB 1; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
Db 102 FPPPP 106  
|||||  
  
RESULT 20  
ZYX\_MOUSE STANDARD; PRT; 564 AA.  
ID ZYX\_MOUSE  
AC Q62523; P70461;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zyxin.  
GN ZYX.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ICR X SWISS WEBSTER;  
RX MEDLINE=97094926; PubMed=8940160;  
RA Macalima T., Otte J., Hensler M.E., Bockholt S.M., Louis H.A.,  
RA Kalf-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.;  
RT "Molecular characterization of human zyxin.";  
RL J. Biol. Chem. 271:31470-31478(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Otte J., Heischmann A., Breier G., Beckerle M.C.; von der Ahe D.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP  
PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT  
MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY  
SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN  
CYTOSKELETON NEAR THE ADHESION PLAQUES.  
CC -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2

CC ZINC IONS.

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CC -----

DR EMBL; Y07711; CAA68984.1; -

DR EMBL; X99063; CAA67510.1; -

DR MGD; MGI-103072; ZYX.

DR InterPro; IPR001781; LIM.

DR Pfam; PF00412; LIM; 3.

DR ProDom; PD000094; LIM; 3.

DR SMART; SM00132; LIM; 3.

DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.

DR PROSITE; PS00023; LIM\_DOMAIN\_2; 3.

DR Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.

DOMAIN 64 77 PRO-RICH.

FT DOMAIN 94 138 PRO-RICH.

FT DOMAIN 376 435 LIM 1.

FT DOMAIN 436 495 LIM 2.

FT DOMAIN 496 562 LIM 3.

FT CONFLICT 215 215 R -> A (IN REF. 1).

FT CONFLICT 284 292 IKKCLRMP -> NQKWPDPD (IN REF. 1).

FT CONFLICT 484 484 S -> C (IN REF. 1).

SQ SEQUENCE 564 AA; 60790 MW; 001E1B3C82ADA1EB CRC64;

Query Match 100.0%; Score 34; DB 1; Length 564;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPPP 5  
| | | | |  
Db 93 FPPPP 97

## RESULT 21

ID ZYX\_HUMAN STANDARD; PRT; 572 AA.

AC Q15942;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

ZYX (zyxin 2).

ZYX.

Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Umbilical vein;

RX MEDLINE=97094926; PubMed=8940160;

RA Macalima T., Otte J., Hensler M.E., Bockholt S.M., Louis H.A.,

RA Kalif-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.;

RT "Molecular characterization of human zyxin.";

RL J. Biol. Chem. 271:31470-31478(1996).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=97075042; PubMed=8917469;

RA Zumbunn J., Trueb B.;

RT "A zyxin-related protein whose synthesis is reduced in virally

RT transformed fibroblasts.";

RL Eur. J. Biochem. 241:657-663(1996).

CC -!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP

CC PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT

CC MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN

CC CYTOSKELETON NEAR THE ADHESION PLAQUES.

CC -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2

CC ZINC IONS.

CC -----

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CC -----

DR EMBL; X94991; CAA64447.1; -

DR EMBL; X95735; CAA65050.1; -

DR HSP; Q05158; IQLI.

DR MIM; 602002; -

DR InterPro; IPR001781; LIM.

DR Pfam; PF00412; LIM; 3.

DR ProDom; PD000094; LIM; 3.

DR SMART; SM00132; LIM; 3.

DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.

DR PROSITE; PS00023; LIM\_DOMAIN\_2; 3.

DR Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.

DOMAIN 64 77 PRO-RICH.

FT DOMAIN 94 137 PRO-RICH.

FT DOMAIN 384 443 LIM 1.

FT DOMAIN 444 503 LIM 2.

FT DOMAIN 504 570 LIM 3.

SQ SEQUENCE 572 AA; 61277 MW; 2833B1EFA260B762 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 572;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPPP 5  
| | | | |  
Db 93 FPPPP 97

## RESULT 22

ID YBX1\_SCHPO STANDARD; PRT; 584 AA.

AC Q10207;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Hypothetical 64.2 kDa protein C17D1.01 in chromosome II.

GN SPBC17D1.01 OR SPBC17D11.09.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI\_TaxID=4896;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Wood V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt R.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Beck A., Reinhardt R., Wood V., Rajandream M.A., Barrell B.G.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

CC -----

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```
-----
CC EMBL; AL031322; CAA20425.1; -
DR EMBL; AL031739; CAA21080.1; -
KW Hypothetical protein.
SQ SEQUENCE 584 AA; 64207 MW; 1F712A2982F59FF4 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 561 FPPPP 565

RESULT 23
ACTA_LISMO
ID ACTA_LISMO STANDARD; PRT; 639 AA.
AC P33379;
  01-FEB-1994 (Rel. 28, Created)
  01-FEB-1994 (Rel. 28, Last sequence update)
  01-MAR-2002 (Rel. 41, Last annotation update)
DE Actin-assembly inducing protein precursor.
GN ACTA OR PRTB OR LMO0204.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Lo28 / Serovar 1/2c;
RC MEDLINE=92104678; PubMed=1309513;
RA Vazquez-Boland J.-A., Kocks C., Dramsi S., Ohayon H., Geoffroy C.,
  Mengaud J., Cossart P.;
RT "Nucleotide sequence of the lecithinase operon of Listeria
  monocytogenes and possible role of lecithinase in cell-to-cell
  spread.";
RL Infect. Immun. 60:219-230(1992).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=92154667; PubMed=1739966;
RA Kocks C., Gouin E., Tabouret M., Berche P., Ohayon H., Cossart P.;
RT "L. monocytogenes-induced actin assembly requires the actA gene
  product, a surface protein.";
RL Cell 68:521-531(1992).
RN [3]
SEQUENCE FROM N.A., AND SEQUENCE OF 30-59.
RP STRAIN=EGD / Serovar 1/2a;
RC MEDLINE=92258410; PubMed=1582425;
RA Domann E., Wehland J., Rohde M., Pistor S., Hartl M., Goebel W.,
  Leimeister-Wachter M., Wuensher M., Chakraborty T.;
RT "A novel bacterial virulence gene in Listeria monocytogenes required
  for host cell microfilament interaction with homology to the
  proline-rich region of vinculin.";
RL EMBO J. 11:1981-1990(1992).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN=EGD-e / Serovar 1/2a;
RC MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
  Raoult F., Berche P., Blocher H., Brandt P., Chakraborty T.,
  Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
  Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
  Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
  Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
  Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
  Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
  Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
  Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
  Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).

RN CHARACTERIZATION.
RX MEDLINE=94155839; PubMed=8112291;
RA Pistor S., Chakraborty T., Niebuhr K., Domann E., Wehland J.;
RT "The ActA protein of Listeria monocytogenes acts as a nucleator
  inducing reorganization of the actin cytoskeleton.";
RL EMBO J. 13:758-763(1994).
CC FUNCTION: VIRULENCE FACTOR REQUIRED FOR HOST CELL MICROFILAMENT
  INTERACTION. IT INDUCES ACTIN ASSEMBLY AROUND THE BACTERIA TO
  ALLOW IT TO MOVE WITHIN THE CYTOPLASM. IT IS INVOLVED IN THE
  ACTIN POLYMERIZATION PROCESS. IT SEEMS TO ACT AS A NUCLEATOR
  THAT INDUCES THE REORGANIZATION OF THE ACTIN CYTOSKELETON.
CC SUBCELLULAR LOCATION: ANCHORED TO THE MEMBRANE.
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  or send an email to license@isb-sib.ch).
CC EMBL; M82881; AAA25269.1; -
DR EMBL; X59723; CAA42407.1; -
DR EMBL; AL591974; CAD00731.1; -
DR PIR; B43868; B43868.
DR PIR; A42090; A42090.
DR ListList; LMO0204; -
KW Virulence; Signal; Transmembrane; Repeat; Complete proteome.
FT SIGNAL 1 29
FT CHAIN 30 639 ACTIN-ASSEMBLY INDUCING PROTEIN.
FT DOMAIN 266 339 PRO-RICH.
FT DOMAIN 264 333 5 X APPROXIMATE TANDEM REPEATS, PRO-RICH.
FT REPEAT 264 298 1.
FT REPEAT 299 333 2.
FT REPEAT 334 378 3 (APPROXIMATE).
FT REPEAT 379 417 4 (APPROXIMATE).
FT REPEAT 418 422 5 (PARTIAL).
FT SITE 360 362 CELL ATTACHMENT SITE (POTENTIAL).
FT TRANSMEM 613 633 POTENTIAL.
FT CONFLICT 465 466 AP -> DR (IN REF. 3).
SQ SEQUENCE 639 AA; 70348 MW; 5A06CF78BC5F3C91 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 265 FPPPP 269

RESULT 24
SCEL_MOUSE
ID SCEL_MOUSE STANDARD; PRT; 653 AA.
AC Q9EQG3; Q9CTT9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Scellin.
GN Scel.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=20564211; PubMed=11112355;
RA Champlaud M.-F., Baden H.P., Koch M., Jin W., Burgeson R.E., Viel A.;
RT "Gene characterization of scellin (SCEL) and protein localization in
  vertebrate epithelia displaying barrier properties.";
```



```
RL Genomics 70:264-268(2000).
RN [2]
RP SEQUENCE OF 1-201 FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Epididymis;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: May function in the assembly or regulation of proteins
CC in the cornified envelope. The LIM domain may be involved in
CC homotypic or heterotypic associations and may function to localize
CC scellin to the cornified envelope (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
CC membrane proteins by transglutaminase.
CC -!- TISSUE SPECIFICITY: Expressed in the upper layers of stratified
CC epithelia, including, ependyma and choroid plexus of the brain
CC ventricles.
CC -!- DEVELOPMENTAL STAGE: Strong expression was seen in 17-17.5 day-old
CC embryos. Expression was also detected in the amnion of 17.5 day-
CC old embryo.
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC
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CC -----
CC EMBL: AF245700; AAG40727.1; -
CC MBL: AK020345; BAB32078.1; -
CC MGD: MGI:1891228; Scel.
CC InterPro: IPR001781; LIM.
CC SMART: SM00132; LIM; 1.
CC PROSITE: PS00478; LIM_DOMAIN_1; FALSE_NEG.
CC PROSITE: PS50023; LIM_DOMAIN_2; 1.
CC LIM domain; Metal-binding; Zinc; Repeat.
CC
CC DOMAIN 584 650
CC LIM 15 X APPROXIMATE TANDEM REPEATS.
CC
CC FT DOMAIN 207 496
CC FT REPEAT 207 226 1.
CC FT REPEAT 227 241 2.
CC FT REPEAT 242 261 3.
CC FT REPEAT 262 281 4.
CC FT REPEAT 282 301 5.
CC FT REPEAT 302 320 6.
CC FT REPEAT 321 340 7.
CC FT REPEAT 341 360 8.
CC FT REPEAT 361 380 9.
CC FT REPEAT 381 398 10.
CC FT REPEAT 399 418 11.
CC FT REPEAT 419 438 12.
CC FT REPEAT 439 458 13.
CC FT REPEAT 459 477 14.
CC FT REPEAT 478 496 15.
CC
CC FT CONFLICT 157 157 T -> R (IN REF. 2).
CC FT CONFLICT 167 168 QS -> PK (IN REF. 2).
CC SQ SEQUENCE 653 AA; 73172 MW; 1EEB8D52DA1ED59 CRC64;
CC
CC Query Match 100.0%; Score 34; DB 1; Length 653;
CC Best Local Similarity 100.0%; Pred. No. 1.8e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 FPPPP 5
CC Db 139 FPPPP 143
CC
CC RESULT 25
CC SCCEL_HUMAN STANDARD; PRT; 668 AA.
CC AC O95171;
CC DT 01-MAR-2002 (Rel. 41, Created)
CC DT 01-MAR-2002 (Rel. 41, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Scellin.
CC GN SCCEL.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 443-457 AND 635-650.
CC RX MEDLINE=99030435; PubMed=9813070;
CC RA Champilaud M.-F., Burgesson R.E., Jin W., Baden H.P., Olson P.F.;
CC RT "cDNA cloning and characterization of scellin, a LIM domain protein
CC of the keratinocyte cornified envelope.";
CC RL J. Biol. Chem. 273:31547-31554(1998).
CC -!- FUNCTION: May function in the assembly or regulation of proteins
CC in the cornified envelope. The LIM domain may be involved in
CC homotypic or heterotypic associations and may function to localize
CC scellin to the cornified envelope.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
CC membrane proteins by transglutaminase.
CC -!- TISSUE SPECIFICITY: Highly expressed in esophagus. It is also
CC expressed in keratinocytes, amniotic tissue, foreskin stratum
CC spinosum and stratum granulosum, hair follicle and nail.
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC
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CC -----
CC EMBL: AF045941; AAC78461.1; -
CC MIM: 604112; -
CC InterPro: IPR001781; LIM.
CC SMART: SM00132; LIM; 1.
CC PROSITE: PS00478; LIM_DOMAIN_1; FALSE_NEG.
CC PROSITE: PS50023; LIM_DOMAIN_2; 1.
CC LIM domain; Metal-binding; Zinc; Repeat.
CC
CC DOMAIN 599 665
CC LIM 16 X APPROXIMATE TANDEM REPEATS.
CC
CC FT DOMAIN 231 543
CC FT REPEAT 231 246 1.
CC FT REPEAT 247 266 2.
CC FT REPEAT 267 286 3.
CC FT REPEAT 287 306 4.
CC FT REPEAT 307 326 5.
CC FT REPEAT 327 346 6.
CC FT REPEAT 347 366 7.
CC FT REPEAT 367 386 8.
CC FT REPEAT 387 406 9.
```

FT REPEAT 407 426 10.  
FT REPEAT 427 445 11.  
FT REPEAT 446 464 12.  
FT REPEAT 465 484 13.  
FT REPEAT 485 503 14.  
FT REPEAT 504 523 15.  
FT REPEAT 524 543 16.  
SQ SEQUENCE 668 AA; 75297 MW; 612BC3686DBA9FB0 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 668;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
| | | | |  
Db 164 FPPPP 168

arch completed: July 7, 2002, 10:17:57  
b time: 264 sec.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:12:48 ; Search time 28.98 Seconds  
(without alignments)  
29.847 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: SPTREMBL19.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_phage.\*  
11: sp\_plant.\*  
12: sp\_rodent.\*  
13: sp\_virus.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	55	4 Q9H355	Q9H355 homo sapien
2	34	100.0	62	4 Q96S31	Q96S31 homo sapien
3	34	100.0	67	10 Q41381	Q41381 senecio odo
4	34	100.0	75	4 Q8UH33	Q8UH33 homo sapien
5	34	100.0	79	4 Q9UBN0	Q9UBN0 homo sapien
6	34	100.0	80	8 Q79357	Q79357 isoetes lac
7	34	100.0	90	5 Q96SP7	Q96SP7 caenorhabdi
8	34	100.0	93	5 Q61649	Q61649 onchocerca
9	34	100.0	97	10 Q41986	Q41986 arabidopsis
10	34	100.0	102	10 Q9SQF5	Q9SQF5 glycine max
11	34	100.0	116	12 Q9YV1	Q9YV1 eyach virus
12	34	100.0	134	10 Q9XIP3	Q9XIP3 arabidopsis
13	34	100.0	135	12 Q68391	Q68391 human cytom
14	34	100.0	142	10 Q94C20	Q94C20 oryza sativ
15	34	100.0	147	11 Q61900	Q61900 mus musculu
16	34	100.0	149	11 Q35327	Q35327 mus musculu

17	34	100.0	154	2 Q9JNZ6	Q9JNZ6 listeria mo
18	34	100.0	155	2 Q9JNZ1	Q9JNZ1 listeria mo
19	34	100.0	157	2 Q9JNZ4	Q9JNZ4 listeria mo
20	34	100.0	159	2 Q9JMY7	Q9JMY7 listeria mo
21	34	100.0	162	12 Q9JGT6	Q9JGT6 porcine ade
22	34	100.0	165	2 Q9JNZ0	Q9JNZ0 listeria mo
23	34	100.0	166	10 Q9C513	Q9C513 arabidopsis
24	34	100.0	168	2 Q9JMY9	Q9JMY9 listeria mo
25	34	100.0	171	11 Q63401	Q63401 rattus norv
26	34	100.0	181	2 Q9JNZ8	Q9JNZ8 listeria mo
27	34	100.0	182	2 Q9JNZ5	Q9JNZ5 listeria mo
28	34	100.0	183	2 Q9JNZ9	Q9JNZ9 listeria mo
29	34	100.0	186	2 Q9JMY8	Q9JMY8 listeria mo
30	34	100.0	186	3 Q9PFX0	Q9PFX0 schizosacch
31	34	100.0	188	5 Q02579	Q02579 helobdella
32	34	100.0	189	16 Q9HE74	Q9HE74 rhizobium 1
33	34	100.0	198	2 Q9JNZ0	Q9JNZ0 listeria mo
34	34	100.0	199	2 Q9JNZ2	Q9JNZ2 listeria mo
35	34	100.0	200	2 Q9XBN4	Q9XBN4 listeria mo
36	34	100.0	201	11 Q9CTT9	Q9CTT9 mus musculu
37	34	100.0	203	2 Q9JNZ3	Q9JNZ3 listeria mo
38	34	100.0	204	10 Q9SGN4	Q9SGN4 arabidopsis
39	34	100.0	210	4 Q9NXX9	Q9NXX9 homo sapien
40	34	100.0	210	5 Q9VEH6	Q9VEH6 drosophila
41	34	100.0	212	10 Q9M313	Q9M313 arabidopsis
42	34	100.0	218	2 Q9JNZ2	Q9JNZ2 listeria mo
43	34	100.0	230	2 Q9JNZ7	Q9JNZ7 listeria mo
44	34	100.0	236	10 Q9M3A2	Q9M3A2 arabidopsis
45	34	100.0	241	10 Q9FJD8	Q9FJD8 arabidopsis
46	34	100.0	245	12 Q9J118	Q9J118 spodoptera
47	34	100.0	247	2 Q9JN01	Q9JN01 listeria mo
48	34	100.0	247	12 Q01342	Q01342 bovine herp
49	34	100.0	253	4 Q9UFM0	Q9UFM0 homo sapien
50	34	100.0	258	4 Q96K23	Q96K23 homo sapien

#### ALIGNMENTS

RESULT 1

Q9H355 PRELIMINARY; PRT; 55 AA.  
AC Q9H355;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PRO1859.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Zhang C., Yu Y., Zhang S., Zhou G., Wei H., Bi J., Dong C., Zai Y.,  
RA Xu W., Gao F., Liu M., He F.;  
RT "Functional prediction of the coding sequences of 11 new genes deduced  
by analysis of cDNA clones from human fetal liver.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF132202; AAG35548.1; -  
SQ SEQUENCE 55 AA; 6169 MW; 31E9CD6C9C924262 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 55;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 51 FPPPP 55

RESULT 2

```
Q96S31
ID Q96S31 PRELIMINARY; PRT; 62 AA.
AC Q96S31;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOPHETICAL 6.4 KDA PROTEIN.
GN GS19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=97207643; PubMed=9054936;
RX Flint J., Thomas K., Micklem G., Raynham H., Clark K., Doggett N.A.,
RA King A., Higgs D.R.;
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL; AE006462; AAK61219.1; -.
KW Hypothetical protein.
SQ SEQUENCE 62 AA; 6448 MW; 36DDE6289E11E26B CRC64;

Query Match 100.0%; Score 34; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 11 FPPPP 15

RESULT 3
Q41381 PRELIMINARY; PRT; 67 AA.
ID Q41381;
AC Q41381;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF (FRAGMENT).
OS Senecio odorus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Senecioneae; Senecio.
OX NCBI_TaxID=34237;
RN [1]
SEQUENCE FROM N.A.
RP Pyee J., Kolattukudy P.E.;
RA "Epidermis-specific transcripts including one that encodes a new class
RT of lipid transfer proteins in Kleinhia odora.";
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L33794; AAA33936.1; -.
FT NON_TER 1
FT SEQUENCE 67 AA; 7815 MW; 836C9D6A37BCD612 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
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DB 48 FPPPP 52

RESULT 4
Q9UH33 PRELIMINARY; PRT; 75 AA.
ID Q9UH33;
AC Q9UH33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DJ106120.3 (RNA BINDING MOTIF PROTEIN 9) (FRAGMENT).
GN RBM9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP Dodsworth S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL079295; CAB62985.1; -.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 7924 MW; E86E2F0A2EB7545B CRC64;

Query Match 100.0%; Score 34; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
DB 21 FPPPP 25

RESULT 5
Q9UBN0 PRELIMINARY; PRT; 79 AA.
ID Q9UBN0;
AC Q9UBN0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROLINE RICH PEPTIDE P-B PRECURSOR (SIMILAR TO PROTEIN HOMOLOGOUS TO
DE SALIVARY PROLINE-RICH PROTEIN P-B).
GN PBII.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE-SUBMAXILLARY GLAND;
RX MEDLINE=80006513; PubMed=479131;
RA Isemura S., Saito E., Sanada K.;
RT "Isolation and amino acid sequences of proline-rich peptides of human
RT whole saliva.";
RL J. Biochem. 86:79-86(1979).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE-SUBMAXILLARY GLAND;
RX MEDLINE=95073971; PubMed=7982889;
RA Isemura S., Saito E.;
RT "Molecular cloning and sequence analysis of cDNA coding for the
RT precursor of the human salivary proline-rich peptide P-.";
RL J. Biochem. 115:1101-1106(1994).
RN [3]
SEQUENCE FROM N.A.
RP Isemura S.;
RA "Nucleotide sequence of gene PBII encoding human salivary proline-rich
RT protein P-B.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=DUODENUM, ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; D29833; BAA06213.1; -.
DR EMBL; AB031740; BAA88517.1; -.
DR EMBL; BC015327; AAHL15327.1; -.
DR InterPro; IPR002965; P-rich_extensn.
DR PRINTS; PRO1217; PRICHEXTENS.
KW SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 79 PROLINE RICH PEPTIDE P-B.
SQ SEQUENCE 79 AA; 8188 MW; 7B10AE90E95ECB61 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FPPPP 5
|||||
72 FPPPP 76

RESULT 6
ID 079357 PRELIMINARY; PRT; 80 AA.
AC 079357;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 1 (FRAGMENT).
GN NADL.
OS Isoetes lacustris.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
OX NCBI_TaxID=50271;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063402; PubMed=9848656;
RA Malek O., Knoop V.;
RT "Trans-splicing in plant mitochondria: The complete set of ancestor
RT introns in ferns, fern allies and a hornwort.";
RL RNA 4:1599-1609(1998).
DR EMBL; Y17812; CAA76886.1; -.
DR InterPro; IPR001694; Resp_chain_NADH_DHL.
DR Pfam; PF00146; NADHdh; 1.
DR Mitochondrion; NAD.
FT NON_TER 1 80
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 8386 MW; 0780753692C5DD55 CRC64;

Query Match 100.0%; Score 34; DB 8; Length 80;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
|||||
DB 15 FPPPP 19

RESULT 7
Q965P7 PRELIMINARY; PRT; 90 AA.
ID Q965P7;
AC Q965P7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN Y22D7AL.3.
GN Y22D7AL.3.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Madsen C.;
RT "The sequence of C. elegans cosmid Y22D7AL.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084153; AAK84592.1; -.
SQ SEQUENCE 90 AA; 9766 MW; E736DF3DCBBE9654 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
|||||
DB 13 FPPPP 17

RESULT 8
ID 061649 PRELIMINARY; PRT; 93 AA.
AC 061649;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PYRROLIDONE-RICH ANTIGEN.
GN OV42.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Titanji V.P.K., Souopgui J., Goghomu S.M., Nde P.N., Lucius R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055985; AAC12760.1; -.
SQ SEQUENCE 93 AA; 9785 MW; 80C2F2EB0DE27D17 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
|||||
DB 55 FPPPP 59

RESULT 9
ID Q41986 PRELIMINARY; PRT; 97 AA.
AC Q41986;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
```

```
DE EXTENSIN (FRAGMENT).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=SEEDLING;
RA Desprez T., Anselme J., Chiapello H., Rouze P., Caboche M., Hofte H.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z18788; CAA79264.1; -.
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENSIN.
FT NON_TER 1
FT NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 10714 MW; E646127A704A3A2C CRC64;

Query Match 100.0%; Score 34; DB 10; Length 97;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 79 FPPPP 83

RESULT 10
Q9SQF5 PRELIMINARY; PRT; 102 AA.
ID AC Q9SQF5
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 11.8 KDA PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PI437654;
RA Mahalingam R., Wang G., Knap H.T.;
RT "Transcriptionally regulated genes in soybean - soybean cyst nematode
interactions.";
RL Submitted (SEP-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098663; AAF03043.1; -.
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENSIN.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 102 AA; 11781 MW; CA06AB2D583D5BC9 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 30 FPPPP 34

RESULT 11
Q9YVY1 PRELIMINARY; PRT; 116 AA.
ID AC Q9YVY1
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE VP12 PROTEIN (FRAGMENT).
```

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OS Eyach virus.
OC Viruses; dsRNA viruses; Reoviridae; Coltivirus.
OX NCBI_TaxID=62352;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EYACH;
RX MEDLINE=98451335; PubMed=9780055;
RA Attoui H., Charrel R.N., Billoy F., Cantaloube J.F., de Micco P.,
RA de Lamballerie X.;
RT "Comparative sequence analysis of American, European and Asian
RT isolates of viruses in the genus Coltivirus.";
RL J. Gen. Virol. 79:0-0(0).
DR EMBL; AF007185; AAC72009.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 116 AA; 12384 MW; FF2D3F45E00DA4F8 CRC64;

Query Match 100.0%; Score 34; DB 12; Length 116;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 82 FPPPP 86

RESULT 12
Q9XIP3 PRELIMINARY; PRT; 134 AA.
ID AC Q9XIP3
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AT2G27390 PROTEIN.
DE AT2G27390.
GN AT2G27390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006233; AAD41991.1; -.
DR InterPro; IPR003882; Pistil_extensin.
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENSIN.
DR PRINTS; PR01218; PSTLEXTENSIN.
SQ SEQUENCE 134 AA; 14279 MW; 472FCE11F99806AB CRC64;

Query Match 100.0%; Score 34; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 11111
```

Db 80 FPPPP 84

## RESULT 13

Q68391 ID Q68391 PRELIMINARY; PRT; 135 AA.  
AC Q68391;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE ORF UL139.  
OS Human cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOLEDO;  
RX Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;  
"Human cytomegalovirus clinical isolates carry at least 19 genes not  
found in laboratory strains.";  
J. Virol. 70:78-83(1996).  
DR EMBL; U33331; AAA85878.1; -.  
SQ SEQUENCE 135 AA; 14026 MW; C776D81FB48E0D31 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 34; DB 12; Length 135;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 130 FPPPP 134

## RESULT 14

Q94CZ0 ID Q94CZ0 PRELIMINARY; PRT; 142 AA.  
AC Q94CZ0;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE P0004A09.10 PROTEIN.  
GN P0004A09.10.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
clone:P0004A09."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003607; BAB63774.1; -.  
SQ SEQUENCE 142 AA; 14914 MW; 7B886969496BD9C4 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 34; DB 10; Length 142;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 111 FPPPP 115

## RESULT 15

Q61900 ID Q61900 PRELIMINARY; PRT; 147 AA.

AC Q61900;  
DT 01-JAN-1999 (TRENBLrel. 09, Created)  
DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE SALIVARY PROTEIN MSGI PRECURSOR.  
GN SMRI OR MSGI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BAIB/C; TISSUE-SUBMAXILLARY GLAND;  
RX MEDLINE=94252564; PubMed=8194749;  
RA Tronik-Le Roux D., Senorale-Pose M., Rougeon F.;  
RT "Three novel SMRI-related cDNAs characterized in the submaxillary  
gland of mice show extensive evolutionary divergence in the protein  
coding region.";  
Gene 142:175-182(1994).  
RL Gene 142:175-182(1994).  
CC - FUNCTION: MAY PLAY A ROLE IN PROTECTION OR DETOXICATION.  
CC - SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC - TISSUE SPECIFICITY: SECRETED INTO SALIVA BY SUBMAXILLARY GLAND.  
DR EMBL; X71629; CAA50636.1; -.  
DR MGD; MGI:102763; Smrl.  
KW Signal; Repeat; Multigene family; Cleavage on pair of basic residues;  
KW Saliva.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 147 SALIVARY PROTEIN MSGI.  
FT PEPTIDE 27 33 SMRI-LIKE PEPTIDE.  
FT DOMAIN 34 41 POLY-PRO.  
FT DOMAIN 43 78 3 X 12 AA TANDEM REPEATS OF  
FT REPEAT 43 54 G-P-G-I-G-R-P-[HP]-P-P-P-[PF].  
FT REPEAT 55 66 1.  
FT REPEAT 67 78 2.  
FT REPEAT 61 65 3.  
FT DOMAIN 73 84 POLY-PRO.  
FT DOMAIN 73 84 POLY-PRO.  
SQ SEQUENCE 147 AA; 15544 MW; 07D64E22F1BF58C2 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 34; DB 11; Length 147;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 35 FPPPP 39

## RESULT 16

Q35327 ID Q35327 PRELIMINARY; PRT; 149 AA.  
AC Q35327;  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE PROLINE-RICH PROTEIN 7 (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Ernekova K., Chang A., Zambrano N., de Candia P., Russo T., Sudol M.;  
RT "Proteins implicated in Alzheimer disease: the role of FE65, a new  
adaptor which binds to beta-amyloid precursor protein.";  
Adv. Exp. Med. Biol. 0:0-0(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98070482; PubMed=9407065;  
RA Ernekova K.S., Zambrano N., Linn H., Minopoli G., Gertler F.,  
Russo T., Sudol M.;  
RT "The WW domain of neural protein FE65 interacts with proline-rich

RT motifs in mena, the mammalian homolog of drosophila enabled.";  
RL J. Biol. Chem. 272:32869-32877(1997).  
DR EMBL; AF020311; AAB94878.1; -.  
FT NON\_TER 149  
SQ SEQUENCE 149 AA; 16993 MW; 1D0BBAAE494781D06 CRC64;

Query Match 100.0%; Score 34; DB 11; Length 149;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPPPP 5  
Db 49 FPPPP 53

## RESULT 17

Q9JWZ6 PRELIMINARY; PRT; 154 AA.  
ID Q9JWZ6  
AC Q9JWZ6; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
GN ACTA.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=730899;  
RX MEDLINE=97342743; PubMed=9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
RT Listeria monocytogenes lineages with differences in pathogenic  
RT potential.";  
RL Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=730899;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281887; AAF82591.1; -.  
FT NON\_TER 154  
SQ SEQUENCE 154 AA; 16828 MW; FDC09822E888E188 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 154;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPPPP 5  
Db 10 FPPPP 14

## RESULT 18

Q9JWZ1 PRELIMINARY; PRT; 155 AA.  
ID Q9JWZ1  
AC Q9JWZ1; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
GN ACTA.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.

OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LL19;  
RX MEDLINE=97342743; PubMed=9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
RT Listeria monocytogenes lineages with differences in pathogenic  
RT potential.";  
RL Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LL19;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281892; AAF82596.1; -.  
FT NON\_TER 155  
SQ SEQUENCE 155 AA; 16946 MW; 21786A2772578C95 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 155;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPPPP 5  
Db 10 FPPPP 14

## RESULT 19

Q9JWZ4 PRELIMINARY; PRT; 157 AA.  
ID Q9JWZ4  
AC Q9JWZ4; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
GN ACTA.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=696073;  
RX MEDLINE=97342743; PubMed=9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
RT Listeria monocytogenes lineages with differences in pathogenic  
RT potential.";  
RL Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=696073;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281889; AAF82593.1; -.  
FT NON\_TER 157  
SQ SEQUENCE 157 AA; 17171 MW; 9621B027CB297AFD CRC64;

Query Match 100.0%; Score 34; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPPPP 5  
Db 11



Db 42 FPPPP 46

## RESULT 20

Q9JMY7  
ID Q9JMY7 PRELIMINARY; PRT; 159 AA.  
AC Q9JMY7;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
GN ACTA.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=457778;  
RX MEDLINE=97342743; PubMed=9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
RT Listeria monocytogenes lineages with differences in pathogenic  
RT potential.";  
RT Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=457778;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281896; AAF82600.1; -;  
FT NON\_TER 1  
FT NON\_TER 159  
SQ SEQUENCE 159 AA; 17496 MW; F762A575D56A774A CRC64;

Query Match 100.0%; Score 34; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 10 FPPPP 14

## RESULT 21

Q9IGT6  
ID Q9IGT6 PRELIMINARY; PRT; 162 AA.  
AC Q9IGT6;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2001 (TremBLrel. 18, Last annotation update)  
DE 162R.  
GN 162R.  
OS Porcine adenovirus type 3 (PAV-3).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=35265;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Aggarwal N., Mittal S.K.;  
RT "Sequence Analysis of Porcine Adenovirus Type 3 El Region, pIX, pIVa2  
RT Genes, and Five Novel Open Reading Frames.";  
RL Intervirology 0:0-0(2000).  
DR EMBL; AF247039; AAF78233.1; -;  
SQ SEQUENCE 162 AA; 15674 MW; FC13A10BB343A612 CRC64;

Query Match

Best Local Similarity 100.0%; Score 34; DB 12; Length 162;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 4 FPPPP 8

## RESULT 22

Q9JMZ0  
ID Q9JMZ0 PRELIMINARY; PRT; 165 AA.  
AC Q9JMZ0;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
GN ACTA.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L83;  
RX MEDLINE=97342743; PubMed=9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
RT Listeria monocytogenes lineages with differences in pathogenic  
RT potential.";  
RT Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L83;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281893; AAF82597.1; -;  
FT NON\_TER 1  
FT NON\_TER 165  
SQ SEQUENCE 165 AA; 18272 MW; COEFE78CCEA860F1 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

|||||

Db 45 FPPPP 49

## RESULT 23

Q9C5I3  
ID Q9C5I3 PRELIMINARY; PRT; 166 AA.  
AC Q9C5I3;  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE PUTATIVE ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4 PROTEIN (ERF  
DE DOMAIN PROTEIN1).  
GN F3M18.20 OR ATERF1.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsiis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
Theologis A.;

RT "Full Length cDNA of gene F3M18.20 (GI:6560756).";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21380424; PubMed-11487705;  
RA Ohta M., Matsui K., Hiratsu K., Shinshi H., Ohme-Takagi M.;  
RT "Repression Domains of Class II ERF Transcriptional Repressors Share  
an Essential Motif for Active Repression.";  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,  
RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,  
RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,  
RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,  
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT "Full Length cDNA of gene F3M18.20 (GI:6560756).";  
RN [4]  
RP Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RA EMBL; AF360232; AAK25942.1; -;  
RA EMBL; AB055882; BAB62911.1; -;  
RA EMBL; AY040032; AAK64090.1; -;  
DR HSP; O80337; ZGCC.  
DR InterPro; IPR001471; AP2-domain.  
DR Pfam; PF00847; AP2-domain; 1.  
DR PRINTS; PD00367; ETHRSPLENT.  
DR ProDom; PD001423; AP2-domain; 1.  
DR SMART; SM00380; AP2; 1.  
SQ SEQUENCE 166 AA; 18612 MW; A327522DB20E5984 CRC64;  
  
Query Match 100.0%; Score 34; DB 10; Length 166;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
Db 160 FPPPP 164  
  
RESULT 24  
QJUNY9 PRELIMINARY; PRT; 168 AA.  
AC QJUNY9;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ACTA (FRAGMENT).  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L99;  
RX MEDLINE-97342743; PubMed-9199440;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RT "Ribotypes and virulence gene polymorphisms suggest three distinct  
Listeria monocytogenes lineages with differences in pathogenic  
potential.";  
RL Infect. Immun. 65:2707-2716(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L99;  
RA Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,  
RA Batt C.A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF281894; AAF82598.1; -;  
FT NON\_TER 1

FT NON\_TER 168  
SQ SEQUENCE 168 AA; 18309 MW; 310F9CAB705EDDB6 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 168;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
Db 45 FPPPP 49  
  
RESULT 25  
Q63401 PRELIMINARY; PRT; 171 AA.  
AC Q63401;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE (CLONE REM2) ORF (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HOLZMAN; TISSUE=BRAIN;  
RX MEDLINE-96235155; PubMed-8642059;  
RA Asakura K., Fogulis R.J., Pease L.R., Rodriguez M.;  
RT "A monoclonal autoantibody which promotes central nervous system  
remyelination is highly polyreactive to multiple known and novel  
RT antigens.";  
RL J. Neuroimmunol. 65:11-19(1996).  
DR EMBL; L41684; AAB05842.1; -;  
FT NON\_TER 1  
FT NON\_TER 171  
SQ SEQUENCE 171 AA; 18947 MW; 36576590383E0581 CRC64;  
  
Query Match 100.0%; Score 34; DB 11; Length 171;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
Db 153 FPPPP 157  
  
Search completed: July 7, 2002, 10:17:24  
Job time: 276 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2002, 10:11:54 ; Search time 28.57 Seconds  
(without alignments)  
19.439 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Al number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_032802.\*

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
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- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	5	AAW37157	EVH1 ligand motif.
2	34	100.0	5	AAW37157	Amino acid sequenc
3	34	100.0	5	AAU09140	Ena/VASP homology
4	34	100.0	6	AAW31441	Transcriptional ac
5	34	100.0	9	AAU09144	Ena/VASP homology
6	34	100.0	10	AAU09138	Ena/VASP homology
7	34	100.0	14	AAW37157	Peptide derived fr
8	34	100.0	15	AAW37157	Synthetic antigeni
9	34	100.0	15	AAW37157	Colostrinin deriv
10	34	100.0	15	AAW37157	Colostrinin peptid
11	34	100.0	15	AAW37157	Colostrinin peptid

12	34	100.0	15	22	AAW37157	Eve colostrinin pe
13	34	100.0	16	22	AAW37157	Eve colostrinin pe
14	34	100.0	17	19	AAW37157	LRP5 protein fragm
15	34	100.0	18	17	AAW37157	SH3-binding peptid
16	34	100.0	18	18	AAW37157	PPPY motif contai
17	34	100.0	18	18	AAW37157	Peptide resembling
18	34	100.0	18	19	AAW37157	Extendin agonist (1
19	34	100.0	18	19	AAW37157	Extendin agonist (2
20	34	100.0	18	19	AAW37157	Extendin agonist (2
21	34	100.0	18	19	AAW37157	Extendin agonist (2
22	34	100.0	18	19	AAW37157	Extendin agonist (1
23	34	100.0	18	19	AAW37157	Extendin agonist (1
24	34	100.0	18	19	AAW37157	Extendin agonist (1
25	34	100.0	18	19	AAW37157	Extendin agonist (3
26	34	100.0	18	20	AAW37157	Extendin agonist co
27	34	100.0	18	20	AAW37157	Extendin agonist co
28	34	100.0	18	20	AAW37157	Extendin agonist co
29	34	100.0	18	20	AAW37157	Extendin agonist co
30	34	100.0	18	20	AAW37157	Extendin agonist co
31	34	100.0	18	20	AAW37157	Extendin agonist co
32	34	100.0	18	20	AAW37157	Extendin agonist co
33	34	100.0	18	21	AAW37157	Extendin agonist c
34	34	100.0	18	21	AAW37157	Extendin agonist c
35	34	100.0	18	21	AAW37157	Extendin agonist c
36	34	100.0	18	21	AAW37157	Extendin agonist c
37	34	100.0	18	21	AAW37157	Extendin agonist c
38	34	100.0	18	21	AAW37157	Extendin agonist c
39	34	100.0	20	19	AAW37157	ActA peptide (aa29
40	34	100.0	20	22	AAW37157	PEST-like amino ac
41	34	100.0	26	22	AAW37157	Human immune/haema
42	34	100.0	28	22	AAW37157	Peptide #4301 enco
43	34	100.0	28	22	AAW37157	Peptide #4369 enco
44	34	100.0	28	22	AAW37157	Protein #4188 enco
45	34	100.0	28	22	AAW37157	Human brain expres
46	34	100.0	28	22	AAW37157	Human bone marrow
47	34	100.0	28	22	AAW37157	Peptide #4279 enco
48	34	100.0	28	22	AAW37157	Peptide #4388 enco
49	34	100.0	28	22	AAW37157	Peptide #4174 enco
50	34	100.0	36	22	AAW37157	Human polypeptide

ALIGNMENTS

RESULT 1  
AAW37157  
ID AAW37157 standard; Peptide; 5 AA.

XX AAW37157;

AC AAW37157;

DT 06-JUL-1998 (first entry)

DE EVH1 ligand motif.

XX Mena protein; mammalian Ena; Enabled; Evt protein; cytoskeleton;

XX cell morphology; cell adhesion; cell differentiation; cell growth;

XX cell motility; mouse; EVH1 ligand.

OS Synthetic.

XX WO9801755-A1.

XX 15-JAN-1998.

PD 03-JUL-1997; 97WO-US11669.

XX 05-JUL-1996; 96US-0675815.

XX (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX Gertler FB, Niebuhr K, Soriano P, Wehland J;

DR WPI; 1998-101197/09.  
XX  
PT Detection of modulators of Mena and Ena-VASP-like genes and proteins  
PT - used in control of cytoskeletal dynamic events in normal and  
PT abnormal cell morphology, adhesion, motility, growth and  
PT differentiation  
XX  
PS Example 7; Page 44; 77pp; English.  
XX  
CC This peptide motif is found in zyxin, vinculin and other focal  
CC adhesion proteins containing an ActA-like motif. The N-terminal  
CC portion of novel murine Mena (mammalian Ena) protein (see AA037148)  
CC contains an Ena-VASP homology domain (EVH1) that directs the proper  
CC localisation of Mena to focal contacts via directed protein-protein  
CC interactions with zyxin, vinculin etc. This suggests that the  
CC FPPPP motif may comprise the core recognition site in EVH1 ligands.  
CC Based on the disclosed Mena and Evl genes (see AA02996-98) and  
CC proteins (see AA037148-53), a variety of methods and compositions are  
CC provided for screening, isolating and characterising endogenous and  
CC exogenous factors, drugs and therapeutic agents useful to evaluate  
CC and/or control cytoskeletal dynamic events involved in normal and  
CC abnormal cell morphology, adhesion, motility, growth and/or  
CC differentiation.  
XX  
SQ Sequence 5 AA;  
Query Match 100.0%; Score 34; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 1 fpppp 5  
RESULT 2  
AAG79177  
ID AAG79177 standard; peptide; 5 AA.  
XX  
AC AAG79177;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Amino acid sequence of a Fyb/SLAP complex inhibitor.  
XX  
KW Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
KW infectious disease; cancer; autoimmune disease; inflammation;  
KW platelet aggregation; wound healing; clotting.  
XX  
OS Homo sapiens.  
XX  
PN WO200174858-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US10753.  
XX  
PR 03-APR-2000; 2000US-194215P.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Krause M, Sechi AS, Gertler FB, Wehland J;  
XX  
DR WPI; 2001-616686/71.  
XX  
PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
PT activation for treating cancer, autoimmune disease, and infectious  
PT disease, comprises contacting with a Fyb/SLAP complex modulator -  
XX

PS Claim 4; Page 56; 79pp; English.  
XX  
CC The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP  
CC proteins are ligands for the EVH1 domains of  
CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The  
CC specification describes a method for modulating cytoskeletal  
CC rearrangement in a cell, or T cell response to T cell receptor  
CC stimulation. The method comprises contacting the cell or T cell with  
CC a Fyb/SLAP complex modulator sufficient to modulate the formation  
CC of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The  
CC method is useful for modulating cytoskeletal rearrangement in a cell  
CC such as a lymphocyte, preferably a T cell, a macrophage or a cell  
CC fragment such as a platelet and for modulating T cell response to a  
CC T cell receptor stimulation. T cell response is increased in a subject  
CC having or at risk of developing infectious disease or cancer and T cell  
CC response is inhibited in a subject having or is at risk of developing an  
CC autoimmune disease or a condition characterized by inflammation. A  
CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
CC increasing platelet aggregation for promoting wound healing or  
CC clotting.  
XX  
SQ Sequence 5 AA;  
Query Match 100.0%; Score 34; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 1 fpppp 5  
RESULT 3  
AAU09140  
ID AAU09140 standard; peptide; 5 AA.  
XX  
AC AAU09140;  
XX  
DT 19-DEC-2001 (first entry)  
XX  
DE Ena/VASP homology (EVH) proline-rich motif #1.  
XX  
KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
KW cancer; ischaemia.  
XX  
OS Listeria monocytogenes.  
XX  
PN WO200174853-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10249.  
XX  
PR 03-APR-2000; 2000US-194564P.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
XX  
DR WPI; 2001-626380/72.  
XX  
PT Regulating cell motility for promoting wound healing and tissue  
PT regeneration, treating, neurodegenerative disease and metastasis, by  
PT inducing or depleting a functional enabled/vasodilator-stimulated  
PT

PT phosphoprotein -  
XX  
PS Example 2; Page 60; 107pp; English.  
XX  
XX The invention relates to a method of preventing mammalian cell migration,  
XX comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
XX phosphoprotein (VASP) or promoting cell migration comprising depleting  
XX functional Ena/VASP protein in the mammalian cell. The method is useful  
XX for preventing or promoting mammalian cell migration, preferably tumour  
XX cell migration in vitro or in vivo and to prevent tumour cell metastasis  
XX in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
XX wound healing, preferably fibroblasts or nerve cells of a tissue type  
XX with the inhibitor to promote actin polymerisation and tissue formation  
XX on a scaffold. The inhibitor is also useful for preventing  
XX neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
XX Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
XX trauma, Huntington's disease, epilepsy, ALS-parkinsonism-dementia  
XX complex, progressive supranuclear palsy, progressive bulbar palsy,  
XX spinouscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
XX cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
XX Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
XX inhibitor is further useful for enhancing learning and memory in a  
XX subject having or at risk of developing a learning disorder such as  
XX Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
XX dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
XX is administered in an amount for inhibiting the activity of Mena in a  
XX synapse. Ena/VASP activator is useful for disrupting learning and memory  
XX and the activator is administered in an amount to promote Ena/VASP  
XX protein-F655 interaction. Inducing the activity of Ena/VASP protein  
XX in immune or haematopoietic cells reduces the ability of the cells to  
XX migrate and this is useful for treating and preventing inflammatory  
XX disorders such as arthritis, allergy, gout, organ transplant,  
XX ulcerative colitis and ischaemic diseases and also for treating cancer  
XX metastasis. The present sequence represents the amino acid sequence  
XX of Ena/VASP homology (EVH) proline-rich motif #1.  
SQ Sequence 5 AA;

Query Match 100.0%; Score 34; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 1 fpppp 5

ULT 4  
31441  
ID AAW31441 standard; Protein; 6 AA.  
XX  
XX AAW31441;  
AC  
XX  
DT 04-AUG-1998 (first entry)  
XX  
DE Transcriptional activator peptide fragment LS46.  
XX  
KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;  
KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;  
KW Gal4; DNA binding domain.  
XX  
XX Synthetic.  
XX  
XX WO9744447-A2.  
PN  
XX  
XX 27-NOV-1997.  
PD  
XX  
XX 02-MAY-1997; 97WO-US07338.  
PF  
XX  
XX 01-MAY-1997; 97US-0017016.  
PR  
XX  
XX 03-MAY-1996; 96US-0017016.  
FT

(HARD ) HARVARD COLLEGE.  
Lu X, Ptashne M, Wu Y;  
WPI; 1998-018502/02.  
N-PSDB; AAV02536.  
New transcriptional activator containing DNA binding domain bound to  
peptide - useful for controlling gene expression, especially in gene  
therapy, and in protein-protein interaction assays, does not inhibit  
other transcription activators  
Example 1; Page 24; 55pp; English.  
AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076  
are fragments used in an assay to determine novel transcriptional  
activators. The method involves the production of transcriptional  
activators comprising of a DNA-binding group and a 6-25 amino acid  
peptide that is covalently bonded to the DNA binding group and does not  
represent a fragment of a natural transcription activator.  
Protein-protein interactions are identified in the assay by fusing a  
DNA-binding domain to a library of DNA fragments and introducing this and  
a fusion of target protein and a polypeptide containing a region of Gal4  
which interacts with Gal4p into a cell containing Gal4p and identifying  
members of the library that interact with the target from activation of  
transcription. Such constructs are used to activate transcription in a  
cell, e.g. for controlling gene activity, particularly in gene therapy  
(e.g. recognizing a site close to a selected therapeutic gene).  
Transcription can be activated without blocking other transcriptional  
activators. They probably act by interacting with a component of the RNA  
polymerase II holoenzyme, Gal41, the strongest known yeast activator,  
which provides a more sensitive assay allowing detection of even weak  
protein-protein interactions. Such activators do not create toxicity  
problems even when overexpressed.  
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 1 fpppp 5

RESULT 5  
AAU09144  
ID AAU09144 standard; peptide; 9 AA.  
XX  
XX AAU09144;  
AC  
XX  
DT 19-DEC-2001 (first entry)  
XX  
DE Ena/VASP homology (EVH) proline-rich motif #3.  
XX  
KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
KW Huntington's disease; ALS-parkinsonism-dementia complex; bulbar palsy;  
KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
KW cancer; ischaemia.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 9  
FT /label= OTHER  
FT /note= "Other = any amino acid"

XX PN WO200174853-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US10249.  
 XX PR 03-APR-2000; 2000US-194564P.  
 XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
 XX DR WPI; 2001-626380/72.  
 XX PT Regulating cell motility for promoting wound healing and tissue  
 XX PT regeneration, treating, neurodegenerative disease and metastasis, by  
 XX PT inducing or depleting a functional enabled/vasodilator-stimulated  
 XX PT phosphoprotein -  
 XX Example 6; Page 66; 107pp; English.  
 XX The invention relates to a method of preventing mammalian cell migration,  
 XX comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
 XX phosphoprotein (VASP) or promoting cell migration comprising depleting  
 XX functional Ena/VASP protein in the mammalian cell. The method is useful  
 XX for preventing or promoting mammalian cell migration, preferably tumour  
 XX cell migration in vitro or in vivo and to prevent tumour cell metastasis  
 XX in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
 XX wound healing, preferably fibroblasts or nerve cells of a tissue type  
 XX with the inhibitor to promote actin polymerisation and tissue formation  
 XX on a scaffold. The inhibitor is also useful for preventing  
 XX neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
 XX Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
 XX trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
 XX complex, progressive supranuclear palsy, progressive bulbar palsy,  
 XX spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
 XX cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
 XX Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
 XX inhibitor is further useful for enhancing learning and memory in a  
 XX subject having or at risk of developing a learning disorder such as  
 XX Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
 XX dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
 XX is administered in an amount for inhibiting the activity of Mena in a  
 XX synapse. Ena/VASP activator is useful for disrupting learning and memory  
 XX and the activator is administered in an amount to promote Ena/VASP  
 XX protein-FE65 interaction. Inducing the activity of Ena/VASP protein  
 XX in immune or haematopoietic cells reduces the ability of the cells to  
 XX migrate and this is useful for treating and preventing inflammatory  
 XX disorders such as arthritis, allergy, gout, organ transplant,  
 XX ulcerative colitis and ischemic diseases and also for treating cancer  
 XX metastasis. The present sequence represents the amino acid sequence  
 XX of Ena/VASP homology (EVH) proline-rich motif #3.  
 XX Sequence 9 AA;

Query Match 100.0%; Score 34; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5

Db 1 fpppp 5

RESULT 6

AAU09138

ID AAU09138 standard; peptide; 10 AA.

XX AC AAU09138;

XX XX

DT 19-DEC-2001 (first entry)  
 XX DE Ena/VASP homology (EVH) consensus binding site.  
 XX KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
 KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
 KW neurodegeneration; Alzheimer's disease; Down Syndrome; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
 KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
 KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
 KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
 KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
 KW cancer; ischaemia.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT Misc-difference 1 /label= Asp, Gly  
 FT FT Misc-difference 7 /label= OTHER  
 FT FT /note= "Other = any amino acid"  
 XX PN WO200174853-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US10249.  
 XX PR 03-APR-2000; 2000US-194564P.  
 XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
 XX DR WPI; 2001-626380/72.  
 XX PT Regulating cell motility for promoting wound healing and tissue  
 XX PT regeneration, treating, neurodegenerative disease and metastasis, by  
 XX PT inducing or depleting a functional enabled/vasodilator-stimulated  
 XX PT phosphoprotein -  
 XX Example 2; Page 59; 107pp; English.  
 XX The invention relates to a method of preventing mammalian cell migration,  
 XX comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
 XX phosphoprotein (VASP) or promoting cell migration comprising depleting  
 XX functional Ena/VASP protein in the mammalian cell. The method is useful  
 XX for preventing or promoting mammalian cell migration, preferably tumour  
 XX cell migration in vitro or in vivo and to prevent tumour cell metastasis  
 XX in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
 XX wound healing, preferably fibroblasts or nerve cells of a tissue type  
 XX with the inhibitor to promote actin polymerisation and tissue formation  
 XX on a scaffold. The inhibitor is also useful for preventing  
 XX neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
 XX Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
 XX trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
 XX complex, progressive supranuclear palsy, progressive bulbar palsy,  
 XX spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
 XX cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
 XX Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
 XX inhibitor is further useful for enhancing learning and memory in a  
 XX subject having or at risk of developing a learning disorder such as  
 XX Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
 XX dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
 XX is administered in an amount for inhibiting the activity of Mena in a  
 XX synapse. Ena/VASP activator is useful for disrupting learning and memory  
 XX and the activator is administered in an amount to promote Ena/VASP  
 XX protein-FE65 interaction. Inducing the activity of Ena/VASP protein  
 XX in immune or haematopoietic cells reduces the ability of the cells to  
 XX migrate and this is useful for treating and preventing inflammatory  
 XX disorders such as arthritis, allergy, gout, organ transplant,



CC ulcerative colitis and ischaemic diseases and also for treating cancer  
CC metastasis. The present sequence represents the amino acid sequence  
CC of Ena/VASP homology (EVH) consensus binding site.  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 34; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
| | | | |  
Db 2 fpppp 6  
  
RESULT 7  
AAG79174  
ID AAG79174 standard; peptide; 14 AA.  
  
AAG79174;  
  
DT 03-JAN-2002 (first entry)  
XX Peptide derived from ActA, and containing EVH1-binding site.  
DE  
XX ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
KW infectious disease; cancer; autoimmune disease; inflammation;  
KW platelet aggregation; wound healing; clotting.  
XX  
OS Listeria monocytogenes.  
XX  
PN WO200174858-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US10753.  
XX  
PR 03-APR-2000; 2000US-194215P.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Krause M, Sechi AS, Gertler FB, Wehland J;  
XX WPI; 2001-616686/71.  
  
Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
activation for treating cancer, autoimmune disease, and infectious  
disease, comprises contacting with a Fyb/SLAP complex modulator -  
  
Example 5; Page 43; 79pp; English.  
  
The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are  
ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated  
phosphoprotein (VASP) proteins. The specification describes a method for  
modulating cytoskeletal rearrangement in a cell, or T cell response to T  
cell receptor stimulation. The method comprises contacting the cell or T  
cell with a Fyb/SLAP complex modulator sufficient to modulate the  
formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein.  
The method is useful for modulating cytoskeletal rearrangement in a cell  
such as a lymphocyte, preferably a T cell, a macrophage or a cell  
fragment such as a platelet and for modulating T cell response to a  
T cell receptor stimulation. T cell response is increased in a subject  
having or at risk of developing infectious disease or cancer and T cell  
response is inhibited in a subject having or is at risk of developing an  
autoimmune disease or a condition characterized by inflammation. A  
composition comprising a Fyb/SLAP complex inhibitor is useful for  
increasing platelet aggregation for promoting wound healing or  
clotting. The present sequence represents a peptide derived from  
ActA, which is used in the course of the invention.

XX Sequence 14 AA;  
  
Query Match 100.0%; Score 34; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FPPPP 5  
| | | | |  
Db 3 fpppp 7  
  
RESULT 8  
AAG79166  
ID AAG79166 standard; peptide; 15 AA.  
XX  
AC AAG79166;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Synthetic antigenic peptide derived from ActA.  
XX  
KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
KW infectious disease; cancer; autoimmune disease; inflammation;  
KW platelet aggregation; wound healing; clotting.  
XX  
OS Synthetic.  
OS Listeria monocytogenes.  
XX  
PN WO200174858-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US10753.  
XX  
PR 03-APR-2000; 2000US-194215P.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Krause M, Sechi AS, Gertler FB, Wehland J;  
XX WPI; 2001-616686/71.  
  
Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
activation for treating cancer, autoimmune disease, and infectious  
disease, comprises contacting with a Fyb/SLAP complex modulator -  
  
Example 1; Page 36; 79pp; English.  
  
The present sequence represents an antigenic peptide derived from ActA.  
polyclonal antibodies raised against this peptide were used to screen  
mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP  
proteins are ligands for the EVH1 domains of  
Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins.  
The specification describes a method for modulating cytoskeletal  
rearrangement in a cell, or T cell response to T cell receptor  
stimulation. The method comprises contacting the cell or T cell with a  
Fyb/SLAP complex modulator sufficient to modulate the formation of a  
complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is  
useful for modulating cytoskeletal rearrangement in a cell such as a  
lymphocyte, preferably a T cell, a macrophage or a cell fragment such  
as a platelet and for modulating T cell response to a T cell receptor  
stimulation. T cell response is increased in a subject having or at  
risk of developing infectious disease or cancer and T cell response  
is inhibited in a subject having or is at risk of developing an  
autoimmune disease or a condition characterized by inflammation. A  
composition comprising a Fyb/SLAP complex inhibitor is useful for  
increasing platelet aggregation for promoting wound healing or  
clotting.

[illegible]

XX 22-FEB-2001.  
PD  
XX  
PF 17-AUG-2000; 2000WO-US22774.  
XX  
PR 17-AUG-1999; 99US-0149633.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Boldogh I;  
XX  
DR WPI; 2001-226545/23.  
XX  
PT Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX Claim 6; Page 21; 35pp; English.  
PS  
XX The present invention relates to a method for promoting neural cell  
differentiation and treating damaged neural cells, using colostrinin and  
colostrinin constituent peptides (e.g. the present peptide) as a neural  
cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
CC  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 34; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
DB 6 fpppp 10  
  
RESULT 12  
AAB59312  
ID AAB59312 standard; Peptide; 15 AA.  
XX  
AC AAB59312;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostrinin peptide fragment A-3.  
XX  
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
central nervous system disorder; dietary supplement; beta-amyloid plaque.  
  
Ovis sp.  
WO200075173-A2.  
14-DEC-2000.  
02-JUN-2000; 2000WO-GB02128.  
02-JUN-1999; 99GB-0012852.  
(REGE-) REGEN THERAPEUTICS PLC.  
Georgiades JA;  
WPI; 2001-071058/08.  
Peptides having an N-terminal amino acid sequence isolated from  
colostrinin for treating e.g. disorders of the central nervous system  
and immune system, viral and bacterial infections, and diseases  
characterized by amyloid plaques -  
Claim 7; Page 27; 63pp; English.  
The present invention provides the sequences of a number of peptides  
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
fragment of colostrum. These peptides can be used in the treatment of  
central nervous system disorders such as senile dementia, Parkinson's  
disease, Alzheimer's disease, psychosis and neurosis, immune system  
disorders such as bacterial and viral infections, to improve the  
development of a child's immune system, as a dietary supplement, and to  
promote the dissolution of beta-amyloid plaques.  
  
Query Match 100.0%; Score 34; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
DB 6 fpppp 10  
  
RESULT 13  
AAB59343  
ID AAB59343 standard; Peptide; 16 AA.  
XX  
AC AAB59343;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostrinin peptide fragment derived sequence #3.  
XX  
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
central nervous system disorder; dietary supplement; beta-amyloid plaque.  
  
Ovis sp.  
WO200075173-A2.  
14-DEC-2000.  
02-JUN-2000; 2000WO-GB02128.  
02-JUN-1999; 99GB-0012852.  
(REGE-) REGEN THERAPEUTICS PLC.  
Georgiades JA;  
WPI; 2001-071058/08.  
Peptides having an N-terminal amino acid sequence isolated from  
colostrinin for treating e.g. disorders of the central nervous system  
and immune system, viral and bacterial infections, and diseases  
characterized by amyloid plaques -  
Claim 8; Page 27; 63pp; English.  
The present invention provides the sequences of a number of peptides  
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
fragment of colostrum. These peptides can be used in the treatment of  
central nervous system disorders such as senile dementia, Parkinson's  
disease, Alzheimer's disease, psychosis and neurosis, immune system  
disorders such as bacterial and viral infections, to improve the  
development of a child's immune system, as a dietary supplement, and to  
promote the dissolution of beta-amyloid plaques.  
  
Query Match 100.0%; Score 34; DB 22; Length 16;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
DB 6 fpppp 10  
  
RESULT 14  
AAB59344  
ID AAB59344 standard; Peptide; 16 AA.  
XX  
AC AAB59344;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostrinin peptide fragment derived sequence #4.  
XX  
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
central nervous system disorder; dietary supplement; beta-amyloid plaque.  
  
Ovis sp.  
WO200075173-A2.  
14-DEC-2000.  
02-JUN-2000; 2000WO-GB02128.  
02-JUN-1999; 99GB-0012852.  
(REGE-) REGEN THERAPEUTICS PLC.  
Georgiades JA;  
WPI; 2001-071058/08.  
Peptides having an N-terminal amino acid sequence isolated from  
colostrinin for treating e.g. disorders of the central nervous system  
and immune system, viral and bacterial infections, and diseases  
characterized by amyloid plaques -  
Claim 9; Page 27; 63pp; English.  
The present invention provides the sequences of a number of peptides  
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
fragment of colostrum. These peptides can be used in the treatment of  
central nervous system disorders such as senile dementia, Parkinson's  
disease, Alzheimer's disease, psychosis and neurosis, immune system  
disorders such as bacterial and viral infections, to improve the  
development of a child's immune system, as a dietary supplement, and to  
promote the dissolution of beta-amyloid plaques.

Db |||||  
7 fpppp 11

RESULT 14  
AAW83313  
ID AAW83313 standard; peptide; 17 AA.  
XX  
AC AAW83313;  
XX  
DT 10-FEB-1999 (first entry)  
XX  
DE LRP5 protein fragment #1.  
XX  
KW LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;  
KW endocytosis; insulin dependent diabetes mellitus; autoimmune disease;  
KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein.  
XX  
OS Homo sapiens.  
XX  
PA W09846743-A1.  
XX  
PD 22-OCT-1998.  
XX  
PF 15-APR-1998; 98WO-CB01102.  
XX  
PR 05-JUN-1997; 97US-0048740.  
PR 15-APR-1997; 97US-0043553.  
XX  
PA (MERI ) MERCK & CO INC.  
PA (WELL ) WELLCOME TRUST LTD.  
XX  
PI Caskey CT, Cox RD, Gerhold D, Hammond H, Hess JW;  
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
PI Phillips MS, Todd JA, Twells RCJ;  
XX  
DR WPI; 1998-594573/50.  
XX

XX New isolated LDL-receptor related protein - used to develop products  
PT for treating, e.g. elevated triglyceride levels, diabetes,  
PT autoimmune disorders, inflammation or Alzheimer's disease  
XX  
PS Claim 20; Page 126; 200pp; English.  
XX

XX The present invention describes LRP5 (low density lipoprotein (LDL)  
CC receptor related protein, previously designated LRP-3). The present  
CC sequence represents a specifically claimed LRP5 protein fragment.  
CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining  
CC if an individual is susceptible to insulin dependent diabetes mellitus  
CC (IDDM). The NAMS or proteins can be used for reducing triglyceride levels  
CC in the serum of an individual. Therapies that affect LRP5 may also be  
CC useful in the treatment of autoimmune diseases such as  
CC glomerulonephritis, diseases and disorders involving disruption of  
CC inflammation and/or antigen presentation, cytokine clearance and/or  
CC endocytosis, viral infection, pathogenic bacterial toxin contamination,  
CC elevation of free fatty acids or hypercholesterolemia, type 2 diabetes,  
CC osteoporosis, Alzheimer's disease and cardiovascular disease. Products  
CC from the present invention can also be used for detection, diagnosis and  
CC drug screening.  
XX  
SQ Sequence 17 AA;

Query Match 100.0%; Score 34; DB 19; Length 17;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 6\*fp PPP 10  
|||||

RESULT 15  
AAW05469  
ID AAW05469 standard; Peptide; 18 AA.  
XX  
AC AAW05469;  
XX  
DT 24-FEB-1998 (first entry)  
XX  
DE SH3-binding peptide bSH3020.  
XX  
KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
KW cellular signalling element; cellular structural element; malignancy;  
KW protein identification; functional domain; protein screening;  
KW cellular signal transduction process; binding peptide.  
XX  
OS Synthetic.  
XX  
PN W09631625-A1.  
XX  
PD 10-OCT-1996.  
XX  
PF 04-APR-1996; 96WO-US04454.  
XX  
PR 03-APR-1996; 96US-0630915.  
PR 07-APR-1995; 95US-0417872.  
XX  
PA (CYTO-) CYTOGEN CORP.  
PA (UYNC-) UNIV NORTH CAROLINA.  
XX  
PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;  
XX  
DR WPI; 1996-465045/46.  
XX

XX Identifying polypeptide(s) having specific functional domain (esp.  
PT SH3 domain) - comprises detecting selective binding to recognition  
PT unit, regardless of sequence homology  
XX  
PS Example; Fig 12B; 174pp; English.  
XX

XX AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding  
CC peptides. These sequences were used as parts of multivalent recognition  
CC unit complexes used in the method of the invention. The method of the  
CC invention is for identifying polypeptides containing functional domains  
CC of interest (especially SH3 domains). It comprises contacting a  
CC multivalent recognition unit (RU) complex with a number of peptides and  
CC identifying polypeptides having a selective binding affinity for the RU  
CC complex. The method is based on functional similarities and does not  
CC rely on sequence similarities. Prior methods only gave limited success  
CC for identifying proteins containing an SH3 domain due to the minimal  
CC sequence homology among known SH3 proteins. Multivalent RU complexes are  
CC particularly suited to screening for polypeptides containing functional  
CC domains that are similar to, but not identical in sequence to, the  
CC original target functional domain. The new method enables proteins  
CC having a common function to be identified. Identification of novel SH3  
CC proteins will be useful for a better understanding of cell growth,  
CC malignancy, signal transduction processes, etc. New candidate drugs can  
CC be identified, and their specificities (e.g. pharmacological activities)  
CC can be assessed using the method of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 34; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 10 fpppp 14  
|||||

RESULT 16  
AAW37677

AAW37677 standard; Peptide; 18 AA.  
XX AC AAW37677;  
XX DT 23-APR-1998 (first entry)  
XX DE PPPPY motif containing peptide BSH3020 used to bind WW domains.  
XX KW Peptide recognition unit; WW domain; cell signalling; growth regulation;  
KW cytoskeleton organisation; targeted drug screening; modulator;  
KW WW domain interaction; YAP protein; dystrophin.  
XX OS Synthetic.  
XX PN W09737223-AL.  
XX PD 09-OCT-1997.  
XX PF 03-APR-1997; 97WO-US05547.  
XX PR 03-APR-1996; 96US-0630916.  
XX PA (CYTO-) CYTOGEN CORP.  
XX PA (UYNC-) UNIV NORTH CAROLINA.  
XX PI Fowlkes DM, Kay BK, Pirozzi G;  
XX PI WPI; 1997-503234/46.  
XX DR Identifying cell signalling and growth regulatory polypeptides by  
XX PT reaction with multivalent recognition complex - polypeptides are  
XX PT useful in targeted drug selection  
XX PS Example 6.3; Fig 7; 220pp; English.  
XX CC Peptides AAW37653-77 contain PPPPY-like motifs. The PPPY motif is  
XX CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
XX CC containing this residue have been shown to bind the YAP WW domain, but  
XX CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
XX CC AAW37653-77 were biotinylated and complexed with alkaline streptavidin,  
XX CC and used in a cross affinity mapping experiment. They were tested for  
XX CC their ability to bind to the 12 individual novel WW domains of WWP1  
XX CC (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which  
XX CC were expressed as glutathione-S-transferase expression proteins. The  
XX CC present peptide, derived from a vinculin protein, does not bind to  
XX CC WW domains of the novel proteins. The WW domain is a small functional  
XX CC domain. Its name is derived from the observation that two tryptophan  
XX CC residues, one in the amino terminal portion of the WW domain and one in  
XX CC the carboxyl terminal portion, are conserved. Most proteins containing  
XX CC WW domains have a function involving cell signalling and growth  
XX CC regulation or the organisation of the cytoskeleton. Polypeptides  
XX CC containing a WW domain are identified by treating a multivalent  
XX CC recognition unit complex that has selective binding affinity for a WW  
XX CC domain, with many polypeptides and identifying those with selective  
XX CC affinity for the complex. Proteins containing WW domains are used for  
XX CC targeted drug screening, i.e. to identify potential modulators of  
XX CC specific WW domain interactions.  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 34; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 10 fpppp 14  
RESULT 17  
AAW38909  
ID AAW38909 standard; peptide; 18 AA.  
XX AC AAW38909;  
XX DT 27-MAR-1998 (first entry)  
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.  
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
XX OS Synthetic.  
XX PN W09730074-AL.  
XX PD 21-AUG-1997.  
XX PF 14-FEB-1997; 97WO-US02298.  
XX PR 16-FEB-1996; 96US-0602999.  
XX PA (CYTO-) CYTOGEN CORP.  
XX PA (UYNC-) UNIV NORTH CAROLINA.  
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
XX PI Sparks AB, Thorn JM;  
XX DR WPI; 1997-424972/39.  
XX CC Src homology region 3 binding peptide - used to activate Src  
XX CC tyrosine kinase(s) and to stimulate immune response by increasing  
XX CC production of certain lymphokine(s), e.g. Interleukin-1  
XX PS Claim 22; Page 90; 131pp; English.  
XX CC The present sequence represents a peptide which resembles a Src homology  
XX CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
XX CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
XX CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
XX CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
XX CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
XX CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
XX CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
XX CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
XX CC binding peptides can be used in the method to identify inhibitors of  
XX CC their binding to their respective SH3 domains, which could be used to  
XX CC modulate the pharmacological activity of proteins or polypeptide  
XX CC containing the SH3 domain. The peptides can also be used to activate  
XX CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
XX CC response by increasing the production of certain lymphokines, e.g.  
XX CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
XX CC conjugated molecule to certain cellular compartments containing Src or  
XX CC Src related proteins.  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 34; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 7 fpppp 11  
RESULT 18  
AAW47567  
ID AAW47567 standard; peptide; 18 AA.  
XX AC AAW47567;  
XX DT 03-JUL-1998 (first entry)

XX DE  
XX  
XX  
KW Exendin agonist (18).  
KW Exendin agonist; gastric motility; gastric emptying; treatment;  
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
KW obesity; Gila monster venom.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 18  
FT /note= "amidated"  
FT  
XX  
PN WO9805351-A1.  
XX  
PD 12-FEB-1998.  
XX  
XX  
PF 08-AUG-1997; 97WO-US14199.  
XX  
PR 08-AUG-1996; 96US-0694954.  
XX  
PA (AMYL-) AMYLIN PHARM INC.  
XX  
PI Bealey NRA, Gedulin B, Prickett KS, Young AA;  
XX  
XX WPI; 1998-145351/13.  
DR  
XX  
PT Regulating gastrointestinal motility using exendins or their  
PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
PT impaired glucose tolerance etc., also in diagnostic investigations  
XX  
PS Example 21; Fig 8; 70pp; English.  
XX  
CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the  
CC biliary tract or sphincter of Oddi), postprandial dumping syndrome  
CC and hyperglycaemia (particularly associated with type 2 diabetes),  
CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
CC exendin agonist is administered to prevent stomach contents passing  
CC into the intestines, then the stomach pumped) and obesity. It can  
CC also be administered to subjects undergoing gastrointestinal  
CC diagnostic investigation, particularly radiological or by magnetic  
CC resonance imaging.  
CC Exendins, components of Gila monster venom, have some sequence  
CC similarity to glucagon-like peptides (GLP). They are GLP agonists  
CC and have been suggested (US5424286) for treatment of diabetes and  
CC prevention of hyperglycaemia.  
XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 34; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 13 fpppp 17  
RESULT 19  
AAW47569  
ID AAW47569 standard; peptide; 18 AA.  
XX  
AC AAW47569;  
XX  
DT 03-JUL-1998 (first entry)  
XX  
DE Exendin agonist (20).  
XX  
KW Exendin agonist; gastric motility; gastric emptying; treatment;

KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
KW obesity; Gila monster venom.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 11  
FT /note= "tert-butylglycine"  
FT Modified-site 18  
FT /note= "amidated"  
XX  
PN WO9805351-A1.  
XX  
PD 12-FEB-1998.  
XX  
XX  
PF 08-AUG-1997; 97WO-US14199.  
XX  
PR 08-AUG-1996; 96US-0694954.  
XX  
PA (AMYL-) AMYLIN PHARM INC.  
XX  
PI Bealey NRA, Gedulin B, Prickett KS, Young AA;  
XX  
XX WPI; 1998-145351/13.  
DR  
XX  
PT Regulating gastrointestinal motility using exendins or their  
PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
PT impaired glucose tolerance etc., also in diagnostic investigations  
XX  
PS Example 23; Fig 8; 70pp; English.  
XX  
CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the  
CC biliary tract or sphincter of Oddi), postprandial dumping syndrome  
CC and hyperglycaemia (particularly associated with type 2 diabetes),  
CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
CC exendin agonist is administered to prevent stomach contents passing  
CC into the intestines, then the stomach pumped) and obesity. It can  
CC also be administered to subjects undergoing gastrointestinal  
CC diagnostic investigation, particularly radiological or by magnetic  
CC resonance imaging.  
CC Exendins, components of Gila monster venom, have some sequence  
CC similarity to glucagon-like peptides (GLP). They are GLP agonists  
CC and have been suggested (US5424286) for treatment of diabetes and  
CC prevention of hyperglycaemia.  
XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 34; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
Db 13 fpppp 17  
RESULT 20  
AAW47571  
ID AAW47571 standard; peptide; 18 AA.  
XX  
AC AAW47571;  
XX  
DT 03-JUL-1998 (first entry)  
XX  
DE Exendin agonist (22).  
XX  
KW Exendin agonist; gastric motility; gastric emptying; treatment;  
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;

```

KW obesity; Gila monster venom.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 18
FT Modified-site 18 /note= "amidated"
FT
XX WO9805351-Al.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 25; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 13 fpppp 17

RESULT 21
AAW47577
ID AAW47577 standard; peptide; 18 AA.
XX
XX AAW47577;
XX
XX 03-JUL-1998 (first entry)
XX
XX Extendin agonist (28).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX
XX Synthetic.
XX

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FH Key Location/Qualifiers
FT Modified-site 14
FT /label= Hyp
FT Modified-site 15
FT /label= Hyp
FT Modified-site 16
FT /label= Hyp
FT Modified-site 17
FT /label= Hyp
FT Modified-site 18
FT /note= "amidated"
XX
XX WO9805351-Al.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 31; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 13 fpppp 17

RESULT 22
AAW47562
ID AAW47562 standard; peptide; 18 AA.
XX
XX AAW47562;
XX
XX 03-JUL-1998 (first entry)
XX
XX Extendin agonist (13).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX

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KW obesity; Gila monster venom.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT Modified-site /note= "pentylglycine"
FT Modified-site 18
FT Modified-site /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 16; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 13 fpppp 17

RESULT 23
AAW47564
ID AAW47564 standard; peptide; 18 AA.
XX
XX AAW47564;
XX
XX 03-JUL-1998 (first entry)
XX
XX Extendin agonist (15).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX

obesity; Gila monster venom.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT Modified-site /note= "pentylglycine"
FT Modified-site 18
FT Modified-site /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 16; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 13 fpppp 17

RESULT 24
AAW47550
ID AAW47550 standard; peptide; 18 AA.
XX
XX AAW47550;
XX
XX 03-JUL-1998 (first entry)
XX
XX Extendin agonist (1).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX
XX Synthetic.
XX
```



```

FH Key      Location/Qualifiers
FT Modified-site      18
XX /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 4; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match      100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FPPPP 5
|||||
13 fpppp 17

RESULT 25
AAW47552
ID AAW47552 standard; peptide; 18 AA.
XX
XX AAW47552;
XX
XX 03-JUL-1998 (first entry)
XX
XX Extendin agonist (3).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX
XX Synthetic.
XX
XX Key      Location/Qualifiers
XX Modified-site      18
XX /note= "amidated"
XX
XX
```

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PN WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 6; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX
XX Sequence 18 AA;

Query Match      100.0%; Score 34; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
   |||||
DB 13 fpppp 17

Search completed: July 7, 2002, 10:12:47
Job time: 53 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2002, 10:11:58 ; Search time 16.27 Seconds  
(without alignments)  
7.506 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	18	3	US-08-630-916A-109
2	34	100.0	18	4	US-08-602-999A-305
3	34	100.0	18	4	US-08-630-915A-165
4	34	100.0	23	1	US-08-268-251-56
5	34	100.0	23	5	PCT-US93-01112-56
6	34	100.0	36	1	US-08-487-359-9
7	34	100.0	36	1	US-08-222-798A-9
8	34	100.0	78	1	US-08-487-359-5
9	34	100.0	78	1	US-08-487-359-7
10	34	100.0	78	1	US-08-222-798A-5
11	34	100.0	78	1	US-08-222-798A-7
12	34	100.0	79	1	US-08-487-359-1
13	34	100.0	79	1	US-08-487-359-2
14	34	100.0	79	1	US-08-487-359-3
15	34	100.0	79	1	US-08-487-359-4
16	34	100.0	79	1	US-08-487-359-6
17	34	100.0	79	1	US-08-487-359-8
18	34	100.0	79	1	US-08-222-798A-1
19	34	100.0	79	1	US-08-222-798A-2
20	34	100.0	79	1	US-08-222-798A-3
21	34	100.0	79	1	US-08-222-798A-4
22	34	100.0	79	1	US-08-222-798A-6
23	34	100.0	79	1	US-08-222-798A-8
24	34	100.0	135	1	US-08-414-926A-13
25	34	100.0	135	2	US-08-926-922-13
26	34	100.0	135	3	US-09-253-682-13
27	34	100.0	135	4	US-09-527-657-13

28	34	100.0	311	4	US-09-179-558-66	Sequence 66, Appl
29	34	100.0	366	3	US-09-176-657-2	Sequence 2, Appli
30	34	100.0	539	3	US-08-557-210A-5	Sequence 5, Appli
31	34	100.0	635	1	US-07-832-855-2	Sequence 2, Appli
32	34	100.0	736	4	US-09-102-528-29	Sequence 29, Appl
33	34	100.0	995	5	PCT-US95-04910-14	Sequence 14, Appl
34	34	100.0	1149	3	US-08-560-005-5	Sequence 5, Appli
35	34	100.0	1149	4	US-09-418-540-5	Sequence 5, Appli
36	34	100.0	1250	1	US-08-441-139-9	Sequence 9, Appli
37	34	100.0	1461	2	US-08-993-228-10	Sequence 10, Appl
38	31	91.2	10	1	US-08-230-047-11	Sequence 11, Appl
39	31	91.2	11	1	US-08-336-343A-26	Sequence 26, Appl
40	31	91.2	11	4	US-08-652-877-23	Sequence 23, Appl
41	31	91.2	11	4	US-08-476-515A-23	Sequence 23, Appl
42	31	91.2	12	3	US-08-630-916A-52	Sequence 52, Appl
43	31	91.2	12	3	US-08-630-916A-88	Sequence 88, Appl
44	31	91.2	12	4	US-08-602-999A-268	Sequence 268, App
45	31	91.2	12	4	US-08-630-915A-144	Sequence 144, App
46	31	91.2	13	3	US-08-630-916A-7	Sequence 7, Appli
47	31	91.2	14	3	US-08-630-916A-56	Sequence 56, Appl
48	31	91.2	15	4	US-08-602-999A-377	Sequence 377, App
49	31	91.2	16	3	US-08-630-916A-11	Sequence 11, Appl
50	31	91.2	17	4	US-08-602-999A-383	Sequence 383, App

ALIGNMENTS

RESULT 1  
US-08-630-916A-109  
; Sequence 109, Application US/08630916A  
; Patent No. 601137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-109

Query Match 100.0%; Score 34; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 10 FPPPP 14

RESULT 2  
US-08-602-999A-305  
; Sequence 305, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-305

Query Match 100.0%; Score 34; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 7 FPPPP 11

RESULT 3  
US-08-630-915A-165  
; Sequence 165, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 165:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-165

Query Match 100.0%; Score 34; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 10 FPPPP 14

RESULT 4  
US-08-268-251-56  
; Sequence 56, Application US/08268251  
; Patent No. 5585475  
; GENERAL INFORMATION:  
; APPLICANT: Jamieson, Gordon A  
; APPLICANT: Dedman, John R  
; APPLICANT: Kaetzel, Marcia A  
; TITLE OF INVENTION: Calmodulin-Binding Peptides  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/268,251

;; FILING DATE: 514  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/831,219  
;; FILING DATE: 06-FEB-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Green, Grant D  
;; REGISTRATION NUMBER: 31,259  
;; REFERENCE/DOCKET NUMBER: 272.001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (510) 601-2706  
;; TELEFAX: (510) 655-3542  
;; INFORMATION FOR SEQ ID NO: 56:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 23 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-268-251-56

Query Match 100.0%; Score 34; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 17 FPPPP 21

RESULT 5  
PCT-US93-01112-56  
;; Sequence 56, Application PC/TUS9301112  
;; GENERAL INFORMATION:  
;; APPLICANT: Jamieson, Gordon A  
;; APPLICANT: Dedman, John R  
;; APPLICANT: Kaetzel, Marcia A  
;; TITLE OF INVENTION: Calmodulin-Binding Peptides  
;; NUMBER OF SEQUENCES: 59  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Chiron Corporation  
;; STREET: 4560 Horton Street  
;; CITY: Emeryville  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94608  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WordPerfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/01112  
;; FILING DATE: 19930208  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/831,219  
;; FILING DATE: 06-FEB-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Green, Grant D  
;; REGISTRATION NUMBER: 31,259  
;; REFERENCE/DOCKET NUMBER: 272.001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (510) 601-2706  
;; TELEFAX: (510) 655-3542  
;; INFORMATION FOR SEQ ID NO: 56:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 23 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide

PCT-US93-01112-56

Query Match 100.0%; Score 34; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 17 FPPPP 21

RESULT 6  
US-08-487-359-9  
;; Sequence 9, Application US/08487359  
;; Patent No. 5633229  
;; GENERAL INFORMATION:  
;; APPLICANT: KOKRYAKOV, VLADIMIR N.  
;; APPLICANT: HAWIG, SYLVIA S.L.  
;; APPLICANT: LEHRER, ROBERT I.  
;; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 2000 Pennsylvania Ave. N.W.  
;; CITY: Washington, D.C.  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 20006-1812  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/487,359  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/222,798  
;; FILING DATE: 05-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 2000-0553.00  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 887-0763  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 36 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-487-359-9

Query Match 100.0%; Score 34; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 21 FPPPP 25

RESULT 7  
US-08-222-798A-9  
;; Sequence 9, Application US/08222798A  
;; Patent No. 5804553  
;; GENERAL INFORMATION:  
;; APPLICANT: KOKRYAKOV, VLADIMIR N.

APPLICANT: HARWIG, SYLVIA S.L.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-798A-9

Query Match 100.0%; Score 34; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 21 FPPPP 25

RESULT 8  
US-08-487-359-5  
Sequence 5, Application US/08487359  
Patent No. 5633229  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,359  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/222,798  
FILING DATE: 05-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-5

Query Match 100.0%; Score 34; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 61 FPPPP 65

RESULT 9  
US-08-487-359-7  
Sequence 7, Application US/08487359  
Patent No. 5633229  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,359  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/222,798  
FILING DATE: 05-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-7

Query Match 100.0%; Score 34; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 61 FPPPP 65

## RESULT 10

US-08-222-798A-5  
; Sequence 5, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA

ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
08-222-798A-5

Query Match 100.0%; Score 34; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 61 FPPPP 65

## RESULT 11

US-08-222-798A-7  
; Sequence 7, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-798A-7

Query Match 100.0%; Score 34; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 61 FPPPP 65

## RESULT 12

US-08-487-359-1  
; Sequence 1, Application US/08487359  
; Patent No. 5633229  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA

ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,359  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/222,798  
FILING DATE: 05-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-1

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 13  
US-08-487-359-2  
Sequence 2, Application US/08487359  
Patent No. 5633229  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,359  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/222,798  
FILING DATE: 05-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-2

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 14  
US-08-487-359-3  
Sequence 3, Application US/08487359  
Patent No. 5633229  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,359  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/222,798  
FILING DATE: 05-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-3

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 15  
US-08-487-359-4  
Sequence 4, Application US/08487359  
Patent No. 5633229  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.



; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,359  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/222,798  
; FILING DATE: 05-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0553.00  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 41  
; OTHER INFORMATION: /note= "This position is Har."  
; US-08-487-359-4

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 16  
US-08-487-359-6  
; Sequence 6, Application US/08487359  
; Patent No. 5633229  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,359  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/222,798  
; FILING DATE: 05-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0553.00  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 69  
; OTHER INFORMATION: /note= "This position is Har."  
; US-08-487-359-6

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 17  
US-08-487-359-8  
; Sequence 8, Application US/08487359  
; Patent No. 5633229  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,359  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/222,798  
; FILING DATE: 05-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0553.00  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-359-8

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 18  
US-08-222-798A-1  
; Sequence 1, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,798A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0553.00  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-798A-1

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 19  
US-08-222-798A-2  
; Sequence 2, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.

APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-798A-2

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
Db 62 FPPPP 66

RESULT 20  
US-08-222-798A-3  
; Sequence 3, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,798A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-798A-3

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
DB 62 FPPPP 66

RESULT 21  
US-08-222-798A-4  
Sequence 4, Application US/08222798A  
Patent No. 5804553  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 41  
OTHER INFORMATION: /note= "This position is Har."

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPPP 5  
DB 62 FPPPP 66

RESULT 22  
US-08-222-798A-6  
Sequence 6, Application US/08222798A  
Patent No. 5804553  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.  
STATE: CA  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,798A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0553.00  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 69  
OTHER INFORMATION: /note= "This position is Har."

US-08-222-798A-6

Query Match 100.0%; Score 34; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5  
DB 62 FPPPP 66

RESULT 23  
US-08-222-798A-8  
Sequence 8, Application US/08222798A  
Patent No. 5804553  
GENERAL INFORMATION:  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: LEHRER, ROBERT I.  
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
NUMBER OF SEQUENCES: 9

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; STATE: CA
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,798A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0553.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-222-798A-8

Query Match 100.0%; Score 34; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 62 FPPPP 66

RESULT 24
US-08-414-926A-13
; Sequence 13, Application US/08414926A
; Patent No. 5721354
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,926A
; FILING DATE: March 31, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserif, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-011/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
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; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.07
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..135
; OTHER INFORMATION: /label= ULL139
; US-08-414-926A-13

Query Match 100.0%; Score 34; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 5
Db 130 FPPPP 134

RESULT 25
US-08-926-922-13
; Sequence 13, Application US/08926922
; Patent No. 5925751
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cserif Attorney at Law
; STREET: 750 Arimo Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserif, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.07
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..135
; OTHER INFORMATION: /label= ULL139
; US-08-926-922-13

Query Match 100.0%; Score 34; DB 2; Length 135;
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Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 130 FPPPP 134

Search completed: July 7, 2002, 10:14:02  
Job time: 124 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2002, 10:16:33 ; Search time 15.88 Seconds  
(without alignments)  
30.255 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	14	41.2	5	B37988	acid proteinase li
2	13	38.2	4	S3508	starvation-induced
3	13	38.2	5	B60274	major protein anti
4	11	32.4	5	PS0324	ribulose-bisphosph
5	10	29.4	3	A43391	TRH-like tripeptid
6	10	29.4	4	A32039	tyrosine-melanocyt
7	10	29.4	4	P0240	Ig heavy chain CRD
8	10	29.4	5	E60274	major protein anti
9	10	29.4	5	P00009	angiotensin-conver
10	7	20.6	3	RHPTO	thyroliberin - Bom
11	7	20.6	3	RUSHT	thyroliberin - pig
12	7	20.6	3	RUSHT	thyroliberin - she
13	7	20.6	3	A32971	thyroliberin - cas
14	7	20.6	3	A33802	thyrotropin-releas
15	7	20.6	3	I78890	tyrosine protein k
16	7	20.6	4	A02147	phagocytosis-stimu
17	7	20.6	4	PL0140	carbon-monoxide de
18	7	20.6	4	S17255	ribosomal protein
19	7	20.6	4	A34626	RPCH-related neuro
20	7	20.6	4	I51049	metallothionein-A
21	7	20.6	4	I54357	schwannomin - mous
22	7	20.6	4	P07675	T-cell receptor be
23	7	20.6	5	H0ROHA	proctolin - Americ
24	7	20.6	5	A60521	glycogen phosphory
25	7	20.6	5	JN0862	peptidyl-dipectida
26	7	20.6	5	JN0860	peptidyl-dipectida
27	7	20.6	5	C41225	copper resistance
28	7	20.6	5	A41225	copper resistance
29	7	20.6	5	E42364	flagellar protein

30	7	20.6	5	2	B22565	R-phycocerythrin al
31	7	20.6	5	2	A60411	proctolin - Atlant
32	7	20.6	5	2	J50319	subesophageal gang
33	7	20.6	5	2	G37196	bradykinin-potenti
34	7	20.6	5	2	S53595	hypothetical prote
35	7	20.6	5	2	S11127	phosphoprotein, bo
36	7	20.6	5	2	P0267	Ig heavy chain CRD
37	7	20.6	5	2	JT0520	Ig kappa chain V-I
38	7	20.6	5	2	P0669	T-cell receptor be
39	7	20.6	5	2	P0714	T-cell receptor be
40	6	17.6	3	3	S68328	blood cell protein
41	6	17.6	4	1	ECXAA	antho-RFamide neur
42	6	17.6	4	2	ECNK	cardioexcitatory n
43	6	17.6	4	2	D41654	hypothetical prote
44	6	17.6	4	2	J01273	neuropeptide Antho
45	6	17.6	4	2	A35779	neuropeptide Antho
46	6	17.6	4	2	A25844	antho-RF amide neu
47	6	17.6	4	2	A60418	FMRFamide - polych
48	6	17.6	4	2	A32480	achatin-I - giant
49	6	17.6	4	2	S39390	myosin-light-chain
50	6	17.6	5	2	A32516	cholecystokinin-5

ALIGNMENTS

RESULT 1

B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C:Accession: B37988  
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Ino, S.; Takeuchi, T.; Kitagaki  
J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase f  
A:Reference number: A37988; MUID:91060608  
A:Accession: B37988  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MUR>

Query Match 41.2%; Score 14; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
Db 3 PP 4

RESULT 2

S3508  
starvation-induced ribonuclease - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S3508  
R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
Plant Mol. Biol. 27, 477-485, 1995  
A:Title: cDNA structure and regulatory properties of a family of starvation-induced r  
A:Reference number: S3506; MUID:95201242  
A:Accession: S3508  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KOE>

Query Match 38.2%; Score 13; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2  
||

Db 1 FP 2

RESULT 3

B60274

major protein antigen MP32 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

C:Accession: B60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A:Title: Isolation and partial characterization of major protein antigens in the culture

A:Reference number: A60274; MUID:91099989

A:Accession: B60274

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 &lt;NAG&gt;

Query Match

Best Local Similarity 38.2%; Score 13; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPP 4

| |

Db 2 PAP 4

RESULT 4

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998

C:Accession: PS0324

R:Tsuigita, A.

submitted to JIPID, April 1993

A:Reference number: PS0206

A:Accession: PS0324

A:Molecule type: protein

A:Residues: 1-5 &lt;TSU&gt;

A:Experimental source: leaf, chlorophyll

Query Match

Best Local Similarity 32.4%; Score 11; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FPPP 4

| |

Db 1 FQAP 4

RESULT 5

A43391

TRH-like tripeptide - alfalfa

C:Species: Medicago sativa (alfalfa)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A43391

R:Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992

A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-

A:Reference number: A43391; MUID:92388092

A:Accession: A43391

A:Molecule type: protein

A:Residues: 1-3 &lt;LAC&gt;

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match

Best Local Similarity 29.4%; Score 10; DB 3; Length 3;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

| |

Db 2 YP 3

RESULT 6

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000

C:Accession: A32039

R:Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact

A:Reference number: A32039; MUID:89123285

A:Accession: A32039

A:Molecule type: protein

A:Residues: 1-4 &lt;HOR&gt;

A:Experimental source: brain

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end

F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 29.4%; Score 10; DB 2; Length 4;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

| |

Db 1 YP 2

RESULT 7

PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0240

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0240

A:Molecule type: DNA

A:Residues: 1-4 &lt;YAM&gt;

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 29.4%; Score 10; DB 2; Length 4;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

| |

Db 1 YP 2

RESULT 8

E60274

major protein antigen MP63 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

C:Accession: E60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A:Title: Isolation and partial characterization of major protein antigens in the cult

A:Reference number: A60274; MUID:91099989

A:Accession: E60274

A:Status: preliminary

A:Molecule type: protein



A:Residues: 1-5 <NAG>

Query Match 29.4%; Score 10; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

DB 2 YP 3

RESULT 9

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N:Alternate names: ficus latex peptide 2

C:Species: Ficus carica (common fig)

C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995

C:Accession: PQ0009

Maruyama, S.; Miyoshi, S.; Tanaka, H.

J. Biol. Chem. 53, 2763-2767, 1989

Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Residues: 1-5 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.4%; Score 10; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

DB 2 YP 3

RESULT 10

RHTDIO

thyroliberin - Bombina orientalis

C:Species: Bombina orientalis

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A90919; A01415

R.Yasunara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A:Reference number: A90919; MUID:76138399

A:Accession: A90919

A:Molecule type: protein

A:Residues: 1-3 <YAS>

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.6%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2

DB 3 P 3

RESULT 11

RHPGT

thyroliberin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A01415

R.Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A:Title: Structure of porcine thyrotropin releasing hormone.

A:Reference number: A90560; MUID:70136150

A:Accession: A01415

A:Molecule type: protein

A:Residues: 1-3 <NAI>

R.Boler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A:Title: The identity of chemical and hormonal properties of the thyrotropin releasin

A:Reference number: A90167; MUID:70039904

A:Contents: annotation

A:Note: biological activities and Rf values (in 17 chromatographic systems) of the sy

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.6%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2

DB 3 P 3

RESULT 12

RHSHT

thyroliberin - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A93750; A01415

R.Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A:Title: The elucidation of the primary structure of the hypothalamic thyroid stimula

A:Reference number: A93750

A:Accession: A93750

A:Molecule type: protein

A:Residues: 1-3 <DES>

R.Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A:Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor

A:Reference number: A93161; MUID:70163386

A:Contents: annotation

A:Note: physicochemical characteristics and biological activities of the natural and

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.6%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2

DB 3 P 3

RESULT 13

A92971

thyroliberin - eastern newt (tentative sequence)

C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A92971; A01415

R.Grimm-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens)

A:Reference number: A92971; MUID:75035605

A:Accession: A92971

A:Molecule type: protein  
A:Residues: 1-3 <GRI>  
A:Note: a peptide with the chromatographic and electrophoretic characteristics of thyrol  
stidine, or glutamic acid  
C:Superfamily: thyroliberin precursor  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.6%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
DB 3 P 3

RESULT 14  
33802  
A:Title: thyrotropin-releasing hormone-like peptide - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A33802  
R:Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.  
J. Biol. Chem. 264, 7788-7791, 1989  
A:Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate comp  
A:Reference number: A33802; MUID:89255196  
A:Accession: A33802  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <COC>  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.6%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
DB 3 P 3

RESULT 15  
78890  
A:Title: Tyrosine protein kinase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: I78890  
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein  
A:Reference number: I58407; MUID:95060800  
A:Accession: I78890  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3 <RES>  
A:Cross-references: GB:L33339; NID:g609536; PID:AAA64432.1; PID:g609538  
C:Genetics:  
A:Gene: p52ntk

Query Match 20.6%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
DB 3 P 3

DB 2 P 2

RESULT 16  
A02147  
A:Title: phagocytosis-stimulating peptide (tuftsin) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 03-Feb-1994  
C:Accession: A02147  
R:Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.  
Biochem. Biophys. Res. Commun. 47, 172-179, 1972  
A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating  
A:Reference number: A02147; MUID:72187087  
A:Accession: A02147  
A:Molecule type: protein  
A:Residues: 1-4 <NIS>  
A:Note: a peptide having the same structure, physical properties, and biological acti  
R:Fidalgo, B.V.; Najjar, V.A.  
Biochemistry 6, 3386-3392, 1967  
A:Reference number: A37502; MUID:68091045  
C:Contents: annotation; immunoglobulin class  
C:Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutro  
n is essential for maximum stimulation of the phagocytic activity of neutrophils.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
DB 3 P 3

RESULT 17  
PL0140  
A:Title: carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrog  
C:Species: Pseudomonas carboxydohydrog  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
C:Accession: PL0140  
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot  
A:Reference number: PL0138; MUID:90055678  
A:Accession: PL0140  
A:Molecule type: protein  
A:Residues: 1-4 <KRA>  
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,  
C:Keywords: oxidoreductase

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
DB 4 P 4

RESULT 18  
S17255  
A:Title: ribosomal protein YmLi, mitochondrial, questionable - yeast (Saccharomyces cerevisiae  
C:Species: Saccharomyces cerevisiae  
A:Variety: strain 07173  
C:Date: 23-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 09-May-1997  
C:Accession: S17255  
R:Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa,  
RFBG Lett. 284, 51-56, 1991  
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr  
A:Reference number: S17255; MUID:91285106  
A:Accession: S17255

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 19

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 19

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 20

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 20

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 21

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I54357  
R:Huynh, D.P.; Nechiporuk, T.; Pulst, S.  
Hum. Mol. Genet. 3, 1075-1079, 1994  
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are  
A:Reference number: 154357; MUID:95072570  
A:Accession: I54357  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <RES>  
A:Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923  
C:Genetics:  
A:Gene: NF2

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 2 P 2

## RESULT 22

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

## RESULT 23

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

A:Molecule type: protein  
A:Residues: 1-4 <GR0>  
C:Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae*.  
C:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.6%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
Db 4 P 4

C;Keywords: neuropeptide

Query Match 20.6%; Score 7; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
Db 4 P 4

#### RESULT 24

A60521  
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N;Alternate names: glycogen phosphorylase b  
C;Species: Liza ramada  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
C;Accession: A60521  
R;Bonamusa, L.; Baanante, I.V.  
omp. Biochem. Physiol. B 95, 295-301, 1990  
;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle  
A;Reference number: A60521; MUID:90227907  
A;Accession: A60521  
A;Molecule type: protein  
A;Residues: 1-5 <BON>  
C;Superfamily: phosphorylase  
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 20.6%; Score 7; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
Db 5 P 5

#### RESULT 25

JN0862  
peptidyl-dipeptidase A inhibitory peptide C112 - striped bonito  
C;Species: Sarda orientalis (striped bonito)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: JN0862  
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
A;Reference number: JN0859; MUID:94080036  
A;Accession: JN0862  
A;Molecule type: protein  
A;Residues: 1-5 <MAT>  
A;Experimental source: intestine  
C;Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.6%; Score 7; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
|  
Db 3 P 3

Search completed: July 7, 2002, 10:19:57  
Job time: 204 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:19:24 ; Search time 12.35 Seconds  
(without alignments)  
15.676 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : SwissProt\_40.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	38.2	5	1 PAP2_PARMA	P81864 pardachirus
2	9	26.5	5	1 EI03_LITRU	P82099 litoria rub
3	7	20.6	3	1 THYL_PIG	P01151 sus scrofa
4	7	20.6	4	1 DCM_L_PSECH	P19916 pseudomonas
5	7	20.6	4	1 RM01_YEAST	P36515 saccharomyc
6	7	20.6	4	1 TUFT_HUMAN	P01858 homo sapien
7	7	20.6	5	1 BPPT_BOTIN	P30425 bothrops in
8	7	20.6	5	1 PRCT_PERAM	P01373 periplaneta
9	7	20.6	5	1 SUGA_ACHDO	P19991 acheta dome
10	6	17.6	4	1 ACHI_ACHFU	P35904 acheta fu
11	6	17.6	4	1 FAR3_HIRME	P42562 hirudo medi
12	6	17.6	4	1 FAR4_HIRME	P42563 hirudo medi
13	6	17.6	4	1 FFA_ANTEL	P58705 anthopleura
14	6	17.6	4	1 FLRF_HIRME	P42561 hirudo medi
15	6	17.6	4	1 FLRN_ANTEL	P58707 anthopleura
16	6	17.6	4	1 FMRE_MACNI	P01162 macrocallis
17	6	17.6	4	1 FYRI_ANTEL	P58706 anthopleura
18	6	17.6	4	1 OCPI_OCTMI	P58648 octopus min
19	6	17.6	5	1 ALI4_CARMA	P81817 carcinus ma
20	6	17.6	5	1 EI04_LITRU	P82100 litoria rub
21	6	17.6	5	1 FARP_ARTTR	P41853 artioposthi
22	6	17.6	5	1 RE11_LITRU	P82070 litoria rub
23	6	17.6	5	1 RE21_LITRU	P82071 litoria rub
24	6	17.6	5	1 RE31_LITRU	P82072 litoria rub
25	6	17.6	5	1 RE32_LITRU	P82073 litoria rub
26	6	17.6	5	1 TPIS_CANFA	P54714 canis fami
27	6	17.6	5	1 UC22_MAIZE	P80628 zea mays (m
28	3	8.8	5	1 PSK_DAUCA	P58261 daucus caro
29	1	2.9	4	1 OCP3_OCTMI	P58649 octopus min
30	1	2.9	5	1 UF01_MOUSE	P38639 mus musculu
31	0	0.0	3	1 GRWW_HUMAN	P01157 homo sapien
32	0	0.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
33	0	0.0	4	1 DCM5_PSECH	P19918 pseudomonas

34 0 0.0 4 1 EOSI\_HUMAN P02731 homo sapien  
35 0 0.0 5 1 BIOA\_CITFR P13071 citrobacter  
36 0 0.0 5 1 BIOB\_CITFR P12997 citrobacter  
37 0 0.0 5 1 TRM3\_ECOLI P13973 escherichia  
38 0 0.0 5 1 UXA4\_CHLTR P38005 chlamydia t

ALIGNMENTS

RESULT 1  
PAP2\_PARMA STANDARD; PRT; 5 AA.  
ID P81864;  
AC P81864;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pardachin II (PXII) (Fragment).  
OS Pardachirus marmoratus (Red sea mores sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleioidae; Soleidae; Pardachirus.  
OX NCBI\_TaxID=31087;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=3782138;  
RA Lazarovici P., Primor N., Loew L.M.;  
RT "Purification and pore-forming activity of two hydrophobic  
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus  
RT marmoratus).";  
RL J. Biol. Chem. 261:16704-16713(1986).  
CC -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT  
CC PROPERTIES: FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS  
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.  
CC -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PARDACHIN FAMILY.  
KW Toxin.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 38.2%; Score 13; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 1 FP 2  
||  
Db 4 FP 5

RESULT 2  
EI03\_LITRU STANDARD; PRT; 5 AA.  
ID P82099;  
AC P82099;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Electrin 3.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoldea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";

RL Aust. J. Chem. 52:0-0(1999).  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES 5 5  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;  
 Amidation.

Query Match 26.5%; Score 9; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FPPP 4  
 Db 1 FVHP 4

RESULT 3  
 THYL\_PIG STANDARD; PRT; 3 AA.  
 ID THYL\_PIG  
 AC P01151;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).  
 OS Sus scrofa (Pig),  
 OS Ovis aries (Sheep),  
 OS Bombina orientalis (Oriental fire-bellied toad), and  
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823, 9940, 8346, 8316;  
 RN [1]  
 SEQUENCE.

RC SPECIES-Pig; TISSUE=Hypothalamus;  
 RX MEDLINE=70136150; PubMed=4984938;  
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;  
 RT "Structure of porcine thyrotropin releasing hormone.";  
 RL Biochemistry 9:1103-1106(1970).  
 RN [2]  
 SEQUENCE.

RC SPECIES-Pig;  
 RX MEDLINE=70039904; PubMed=4982117;  
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
 RT "The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamyl-histidyl-proline amide.";  
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
 RN [3]  
 SEQUENCE.

RC SPECIES=Sheep; TISSUE=Hypothalamus;  
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R., Ward D.N.;  
 RT "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass spectrometry.";  
 RL Org. Mass Spectrom. 5:221-228(1971).  
 RN [4]  
 SEQUENCE.

RC SPECIES=Sheep;  
 RX MEDLINE=70163386; PubMed=4985794;  
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W., Guillemin R.;  
 RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.";  
 RL Nature 226:321-325(1970).  
 RN [5]  
 SEQUENCE.

RC SPECIES=B. orientalis; TISSUE=Skin;  
 RX MEDLINE=76138399; PubMed=815011;  
 RA Yasuhara T., Nakajima T.;  
 RT "After: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
 RL Chem. Pharm. Bull. 23:3301-3303(1975).  
 RN [6]  
 SEQUENCE.

RC SPECIES=N. Viridescens;  
 RX MEDLINE=75035605; PubMed=4214528;  
 RA Grimm-Joergensen Y., McKelvy J.F.;  
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";  
 RT J. Neurochem. 23:471-478(1974).  
 CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
 DR PIR; A01415; RHPGT.  
 DR PIR; A93750; RHSHT.  
 DR PIR; A90919; RHTDIO.  
 DR PIR; A92971; A92971.  
 KW Amidation.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 3 3 AMIDATION.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 20.6%; Score 7; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
 Db 3 P 3

RESULT 4  
 DCML\_PSECH STANDARD; PRT; 4 AA.  
 ID DCML\_PSECH  
 AC P19916;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (Fragment).  
 OS Pseudomonas carboxydohydrogena.  
 OC Bacteria; Proteobacteria.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 SEQUENCE.

RC MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in carboxydophilic bacteria.";  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.  
 CC -!- COFACTOR: MOLYBDENUM.  
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.  
 CR PIR; PL0140; PL0140.  
 KW Oxidoreductase; Molybdenum.  
 FT NON\_TER 4 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 20.6%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 P 2  
 Db 4 P 4

RESULT 5  
 RM01\_YEAST STANDARD; PRT; 4 AA.  
 ID RM01\_YEAST  
 AC P36515;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).  
 GN MRPL1.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OX Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91285106; PubMed=2060626;  
 RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,  
 RA Kitakawa M.;  
 RT "Extended N-terminal sequencing of proteins of the large ribosomal  
 RT subunit from yeast mitochondria.";  
 RL FEBS Lett. 284:51-56(1991).  
 DR PIR; S17255; S17255.  
 DR SGD; L0002681; MRPL1.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 4  
 SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;  
  
 Query Match 20.6%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 P 2  
 DB 4 P 4  
  
 RESULT 6  
 TUFT\_HUMAN  
 ID TUFT\_HUMAN STANDARD; PRT; 4 AA.  
 AC P01858;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phagocytosis-stimulating peptide (Tuftsin).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72187087; PubMed=4112769;  
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;  
 RA "The characteristics, isolation and synthesis of the phagocytosis  
 RA stimulating peptide tuftsin.";  
 RA Biochem. Biophys. Res. Commun. 47:172-179(1972).  
 RN [2]  
 RP IMMUNOGLOBULIN CLASS.  
 RX MEDLINE=68091045; PubMed=4169272;  
 RA Fidalgo B.V., Najjar V.A.;  
 RA "The physiological role of the lymphoid system. VI. The stimulatory  
 RA effect of leucophilic gamma globulin (leucokinin) on the phagocytic  
 RA activity of human polymorphonuclear leucocyte.";  
 RL Biochemistry 6:3386-3392(1967).  
 CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE  
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE  
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.  
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTTIC  
 CC ACTIVITY OF NEUTROPHILS.  
 DR PIR; A02147; A02147.  
 DR MIM; 191150; -.  
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;  
  
 Query Match 20.6%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 P 2

Db 3 P 3  
  
 RESULT 7  
 BPP7\_BOTIN  
 ID BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE  
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF  
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
 DR PIR; G37196; G37196.  
 KW Hypotensive agent; Venom.  
 FT MOD\_RES 1  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;  
  
 Query Match 20.6%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 P 2  
 DB 5 P 5  
  
 RESULT 8  
 PRCT\_PERAM  
 ID PRCT\_PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach).  
 OS Limulus polyphemus (Atlantic horseshoe crab), and  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blattodea; Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 6850, 6759;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 RT in insects.";  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=81225865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;

RT "Pentapeptide (proctolin) associated with an identified neuron."  
RL Science 213:567-569(1981).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.polyphemus;  
RX MEDLINE=90287800; PubMed=2356151;  
RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
RA Watson W.H., III, Hunt D.F., Griffin P.R., Alexander J.E.,  
RA Shabanowitz J.;  
RT Identification of proctolin in the central nervous system of the  
RT horseshoe crab, Limulus polyphemus.;  
RL Peptides 11:205-211(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=C.maenas;  
RX MEDLINE=86232789; PubMed=2872661;  
RA Stangier J., Dirksen H., Keller R.;  
RT Identification and immunocytochemical localization of proctolin in  
RT pericardial organs of the shore crab, Carcinus maenas.;  
RL Peptides 7:67-72(1986).  
RN [5]  
RT "FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
RT MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
RL -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
CC THE CRAB PERICARDIAL ORGANS.  
CC  
DR PIR; A01644; HOROHA.  
DR PIR; A60411; A60411.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
  
Query Match 20.6%; Score 7; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 P 2  
Db 4 P 4  
  
RESULT 9  
SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P1991;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Suboesophageal ganglion pentapeptide.  
OS Acheta domesticus (House cricket).  
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
CC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;  
CC Gryllinae; Acheta.  
OX NCBI\_TaxID=6997;  
RN [1]  
RP SEQUENCE.  
RA Wicker C., Wicker C.;  
RT "Isolation and structure of a peptide isolated from the  
RT suboesophageal ganglion of Acheta domesticus (orthoptera).";  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
CC GANGLIA.  
DR PIR; JS0319; JS0319.  
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDB0000000 CRC64;  
  
Query Match 20.6%; Score 7; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 P 2  
Db 4 P 4

RESULT 10  
ACH1\_ACHFU STANDARD; PRT; 4 AA.  
AC P35904;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Achatin-I.  
OS Achatina fulica (Giant African snail).  
CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
CC Achatinacea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN=FERUSSAC; TISSUE=Ganglion;  
RX MEDLINE=89273551; PubMed=2597281;  
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
RT fulica Ferussac containing a D-amino acid residue.";  
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;  
RX MEDLINE=91264856; PubMed=1675568;  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
RT "Purification of achatin-I from the atria of the African giant snail,  
RT Achatina fulica, and its possible function.";  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwashita T., Nomoto K.;  
RT "Crystal structure and molecular conformation of achatin-I  
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuroexcitatory peptide  
RT containing a D-amino acid residue.";  
RL Int. J. Pept. Protein Res. 39:258-264(1992).  
CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
DR PIR; A32480; A32480.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
  
Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1  
Db 2 F 2  
  
RESULT 11  
FAR3\_HIRME STANDARD; PRT; 4 AA.  
AC P42562;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide YLRFF-amide.  
OS Hirudo medicinalis (Medicinal leech).  
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE.



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RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 4 F 4

RESULT 12
ID F4R4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 616 MW; 69D4068B300000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 F 1
4 F 4

DB

RESULT 13
ID FFK4_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthearia; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylacetyl-L-phenyl-Lys-Ala-NH2 (Antho-KAamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

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RN FUNCTION.
RX PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A00000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 14
ID FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX SPECIES-H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RX SPECIES-H.trivolvis; TISSUE-Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 15
ID FLRN_ANTEL

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ID FLRN ANTEL STANDARD; PRT; 4 AA.  
AC P58707;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Antho-RNamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE, AND MASS-SPECTROMETRY.  
RX PubMed=1973541;  
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
RT anemone neuropeptide containing an unusual amino-terminal blocking  
RT group.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron-specific.  
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 1 1 L-3-PHENYLLACTYL.  
FT MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;  
  
Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1  
Db 1 F 1  
  
RESULT 16  
FMRF\_MACNI  
ID FMRF MACNI STANDARD; PRT; 4 AA.  
AC P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE FMRFamide (peak C) (Cardioexcitatory neuropeptide).  
OS Macrocallista nimbosa (Sun-ray clam),  
OS Nereis virens (Sandworm),  
OS Hirudo medicinalis (Medicinal leech), and  
OS Helisoma trivolvis (Shall).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Veneroidea; Veneridae; Macrocallista.  
OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;  
RX MEDLINE=77215956; PubMed=87758;  
RA Price D.A., Greenberg M.J.;  
RT "Structure of a molluscan cardioexcitatory neuropeptide.";  
RL Science 197:670-671(1977).  
RN [2]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
RX MEDLINE=78012038; PubMed=909875;  
RA Price D.A., Greenberg M.J.;  
RT "Purification and characterization of a cardioexcitatory neuropeptide  
RT from the central ganglia of a bivalve mollusc.";  
RL prep. Biochem. 7:261-281(1977).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=N.virens;  
RX MEDLINE=90259866; PubMed=2342992;  
RA Krajniak K.G., Price D.A.;  
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";

RL Peptides 11:75-77(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=H.medicinalis;  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=H.trivolvis; TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
RT trivolvis.";  
RL Peptides 15:31-36(1994).  
CC -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL  
CC ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF  
CC CARDIAC CONTRACTION.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A01426; ECNK.  
DR PIR; A60418; A60418.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A000000000 CRC64;  
  
Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1  
Db 1 F 1  
  
RESULT 17  
FYRL ANTEL  
ID FYRL ANTEL STANDARD; PRT; 4 AA.  
AC P58706;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Antho-RNamide I (Contains: Antho-RNamide II).  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
RA Grimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its  
RT des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";  
RL Peptides 12:1165-1173(1991).  
RN [2]  
RP FUNCTION.  
RX PubMed=8397415;  
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
RT "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-RNamide and Antho-RNamide.";  
RL Proc. R. Soc. Lond. B, Biol. Sci. 253:183-188(1993).  
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron-specific.  
KW Neuropeptide; Amidation.  
FT CHAIN 1 4 ANTHO-RNAMIDE I.  
FT CHAIN 2 4 ANTHO-RNAMIDE II.

FT MOD\_RES 1 1 L-3-PHENYLLACTYL.  
MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 598 MW; 60441B59A000000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 1 F 1

RESULT 18  
OCPI\_OCTMI STANDARD; PRT; 4 AA.  
AC P58648;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DE Cardioactive peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;  
OC Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=89766;  
RN [1]  
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX PubMed=10876044;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor";  
RL Peptides 21:623-630(2000).  
CC -I- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-2 is a 1000 time less  
CC active than Ocp-1.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- PTM: Ocp-2 has L-Phe instead of D-Phe.  
CC -I- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA; 394 MW; 6AA879C81000000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 F 1  
2 F 2

Db 1 F 1

RESULT 19  
AL14\_CARMA STANDARD; PRT; 5 AA.  
ID AL14\_CARMA  
AC P81817;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 14.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;

FT MOD\_RES 1 1 L-3-PHENYLLACTYL.  
MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 598 MW; 60441B59A000000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 1 F 1

RESULT 20  
EI04\_LITRU STANDARD; PRT; 5 AA.  
ID EI04\_LITRU  
AC P82100;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Electrin 4.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella";  
RL Aust. J. Chem. 52:0-0(1999).  
CC -I- SUBCELLULAR LOCATION: SECRETED.  
KW Amphibian skin; Amidation.  
FT MOD\_RES 5 5 AMIDATION.  
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A0000000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 1 F 1

RESULT 21  
FARP\_ARTTR STANDARD; PRT; 5 AA.  
ID FARP\_ARTTR  
AC P41853;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide RYRF-amide.  
OS Artiposthia triangulata.  
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;  
OC Rhabditophora; Seriata; Tricladida; Terricola; Geoplanidae;  
OC Arthurdendyus  
OX NCBI\_TaxID=132421;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=94211927; PubMed=7909164;  
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;  
RT "RYRFamide: a turbellarian FMRFamide-related peptide (FARP).";

RL Regul. Pept. 50:37-43(1994).  
CC -!- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 5 5 AMIDATION.  
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

QY 1 F 1  
Db 5 F 5

RESULT 22  
RE31\_LITRU STANDARD; PRT; 5 AA.  
ID RE31\_LITRU  
AC P82070;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Rubellidin 1.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australin red tree frog  
RT 'Litoria rubella', the skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
CC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

QY 1 F 1  
Db 3 F 3

RESULT 23  
RE21\_LITRU STANDARD; PRT; 5 AA.  
ID RE21\_LITRU  
AC P82071;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Rubellidin 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,

RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australin red tree frog  
RT 'Litoria rubella', the skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
CC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

QY 1 F 1  
Db 3 F 3

RESULT 24  
RE31\_LITRU STANDARD; PRT; 5 AA.  
ID RE31\_LITRU  
AC P82072;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Rubellidin 3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australin red tree frog  
RT 'Litoria rubella', the skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
CC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.  
KW Amphibian skin; Amidation.  
FT MOD\_RES 5 5 AMIDATION.  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

QY 1 F 1  
Db 3 F 3

RESULT 25  
RE32\_LITRU STANDARD; PRT; 5 AA.  
ID RE32\_LITRU  
AC P82073;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Rubellidin 3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litori electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
CC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 570 MW; 71A9C862A00000 CRC64;

Query Match 17.6%; Score 6; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 3 F 3

Search completed: July 7, 2002, 10:23:39  
Job time: 255 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:18:49 ; Search time 28.4 Seconds  
(without alignments)  
30.457 Million cell updates/sec

Title: US-09-825-144-15  
Perfect score: 34  
Sequence: 1 FPPPP 5

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 9  
Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : SPTREMBL19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertibrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archheap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	26.5	5	13 P82099	P82099 litoria rub
2	6	17.6	5	13 P82070	P82070 litoria rub
3	6	17.6	5	13 P82071	P82071 litoria rub
4	6	17.6	5	13 P82072	P82072 litoria rub
5	6	17.6	5	13 P82073	P82073 litoria rub
6	6	17.6	5	13 P82100	P82100 litoria rub
7	0	0.0	4	11 Q08433	Q08433 rattus norv
8	0	0.0	5	2 P83073	P83073 bacillus ce
9	0	0.0	5	10 Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1  
P82099

```
ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 26.5%; Score 9; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 1 FVHP 4

RESULT 2
P82070 PRELIMINARY; PRT; 5 AA.
ID P82070
AC P82070;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTI-BIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=Fab.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 17.6%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 3 F 3

RESULT 3
```

P82071 ID P82071 PRELIMINARY; PRT; 5 AA.  
AC P82071;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE RUBELLIDIN 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECRETION;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella', the skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC -!- ANTIBIOTIC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;  
  
Query Match 17.6%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.6e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1  
Db 3 F 3  
  
RESULT 4  
P82072 ID P82072 PRELIMINARY; PRT; 5 AA.  
AC P82072;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE RUBELLIDIN 3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECRETION;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella', the skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC -!- ANTIBIOTIC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.  
KW Amphibian skin; Amidation.  
FT MOD\_RES 5 5  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;  
  
Query Match 17.6%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.6e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 3 F 3  
  
RESULT 5  
P82073 ID P82073 PRELIMINARY; PRT; 5 AA.  
AC P82073;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE RUBELLIDIN 3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litori electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC -!- ANTIBIOTIC ACTIVITY.  
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
  
Query Match 17.6%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.6e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1  
Db 3 F 3  
  
RESULT 6  
P82100 ID P82100 PRELIMINARY; PRT; 5 AA.  
AC P82100;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE ELECTRIN 4.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litori electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD\_RES 5 5  
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;  
  
Query Match 17.6%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.6e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 F 1



Db 1 F 1

## RESULT 7

Q08433 PRELIMINARY; PRT; 4 AA.  
 AC Q08433;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE, MICROSMAL (EC 2.4.1.17) (UDPGT)  
 DE (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GUNN;  
 MEDLINE=91282758; PubMed=1840486;  
 Sato H., Aono S., Kashiwamata S., Koiwai O.;  
 "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 hyperbilirubinemic Gunn rat.";  
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -!- SUBCELLULAR LOCATION: MICROSOME.  
 DR EMBL; S38636; AAB19259.1; -;  
 KW Transferase; Glycosyltransferase; Microsome; Multigene family.  
 FT NON\_TER 1 1  
 FT NON\_TER 4 4  
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 5.6e+05; Mismatches 0; Gaps 0;

Matches 0; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 F 1

Db 1 N 1

## RESULT 8

P83073 PRELIMINARY; PRT; 5 AA.  
 P83073;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE 88 KDA PROTEIN (FRAGMENT).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-NCIMB 11796;  
 RA Browne N., Dows B.C.A.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 5.6e+05; Mismatches 0; Gaps 0;

Matches 0; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 F 1

Db 1 M 1

## RESULT 9

Q99007 PRELIMINARY; PRT; 5 AA.  
 AC Q99007;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).  
 GN AMY1.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;  
 RX MEDLINE=91329704; PubMed=1831055;  
 RA Jacobsen J.V., Close T.J.;  
 "Control of transient expression of chimaeric genes by gibberellic  
 RT acid and abscisic acid in protoplasts prepared from mature barley  
 RT aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721(1991).  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN  
 CC BARLEY.  
 DR EMBL; X54643; CAA38455.1; -;  
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;  
 KW Calcium; Multigene family.  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;

Best Local Similarity 0.0%; Pred. No. 5.6e+05; Mismatches 0; Gaps 0;

Matches 0; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 F 1

Db 1 M 1

Search completed: July 7, 2002, 10:23:04

Job time: 255 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:14:03 ; Search time 26.88 Seconds  
(without alignments)  
20.661 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

al number of hits satisfying chosen parameters: 21101

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_032802.\*

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6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
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12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	5	AAW37157	EVH1 ligand motif.
2	34	100.0	5	AAW37157	Amino acid sequenc
3	34	100.0	5	AAU09140	Ena/VASP homology
4	28	82.4	4	AAAR80051	Peptidase substrat
5	28	82.4	4	AAAR80057	Peptidase substrat
6	28	82.4	4	AAAR80048	Peptidase substrat
7	28	82.4	4	AAW59261	WW domain ligand p
8	28	82.4	5	AAAR97694	pppy motif found
9	28	82.4	5	AAW37648	Peptide #67 from p
10	28	82.4	5	AAW65842	Daucus carota SERK
11	28	82.4	5	AAW47014	

12	28	82.4	5	19	AAW37156	Mammalian Ena (Men
13	28	82.4	5	20	AAW98982	FAW-(pro)4-Lys(eps
14	28	82.4	5	22	AAU09141	Ena/VASP homology
15	28	82.4	5	22	AAW78309	"L domain" amino a
16	28	82.4	5	22	AAW63123	Amino acid sequenc
17	27	79.4	5	22	AAW72257	Colostrinin derive
18	27	79.4	5	22	AAW72510	Colostrinin peptid
19	27	79.4	5	22	AAW72542	Colostrinin peptid
20	27	79.4	5	22	AAW59320	Eve colostrinin pe
21	24	70.6	4	22	AAW91724	Opioid peptide SEQ
22	24	70.6	5	22	AAW30650	Trypsin modulating
23	21	61.8	4	15	AAW45397	Prolyl endopeptida
24	21	61.8	4	16	AAW80046	Peptidase substrat
25	21	61.8	4	16	AAW80049	Peptidase substrat
26	21	61.8	4	16	AAW80050	Peptidase substrat
27	21	61.8	4	16	AAW80052	Peptidase substrat
28	21	61.8	4	16	AAW80053	Peptidase substrat
29	21	61.8	4	16	AAW80054	Peptidase substrat
30	21	61.8	4	22	AAW46963	High axial ratio m
31	21	61.8	5	15	AAW45396	Prolyl endopeptida
32	21	61.8	5	17	AAW06981	Synthetic peptide
33	21	61.8	5	17	AAW06982	Synthetic peptide
34	21	61.8	5	18	AAW10819	Hepatitis antigen
35	21	61.8	5	18	AAW16485	N-acetylgalactosam
36	21	61.8	5	18	AAW16486	N-acetylgalactosam
37	21	61.8	5	20	AAW86009	Peptide used in th
38	21	61.8	5	22	AAW98211	Recombined interle
39	20	58.8	4	3	AAW20039	Peptide for use in
40	20	58.8	4	20	AAW42629	Murine melanoma an
41	20	58.8	5	5	AAW40642	Sequence of Trp-co
42	20	58.8	5	5	AAW40646	Sequence of Trp-co
43	20	58.8	5	5	AAW40647	Sequence of Trp-co
44	20	58.8	5	5	AAW40419	Animal growth prom
45	20	58.8	5	16	AAW76134	hML(2-6). Homo sa
46	20	58.8	5	19	AAW65835	Peptide #60 from p
47	20	58.8	5	19	AAW65836	Peptide #61 from p
48	20	58.8	5	19	AAW65840	Peptide #65 from p
49	20	58.8	5	19	AAW65796	Polypolyri inhibit
50	20	58.8	5	20	AAW42926	Portion of the cor

#### ALIGNMENTS

RESULT 1  
AAW37157  
ID AAW37157 standard; Peptide; 5 AA.

AC AAW37157;

XX 06-JUL-1998 (first entry)

DE EVH1 ligand motif.

XX Mena protein; mammalian Ena; Enabled; Evi protein; cytoskeleton;  
KW cell morphology; cell adhesion; cell differentiation; cell growth;  
KW cell motility; mouse; EVH1 ligand.

OS Synthetic.

XX WO9801755-A1.

XX 15-JAN-1998.

XX 03-JUL-1997; 97WO-US11669.

XX 05-JUL-1996; 96US-0675815.

XX (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA BOP activated pept

XX Gertler FB, Niebuhr K, Soriano P, Wehland J;



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PT  phosphoprotein
XX
PS  Example 2; Page 60; 107pp; English.
XX
CC  The invention relates to a method of preventing mammalian cell migration,
CC  comprising inducing a functional Ena(enabled)/vasodilator-stimulated
CC  phosphoprotein (VASP) or promoting cell migration comprising depleting
CC  functional Ena/VASP protein in the mammalian cell. The method is useful
CC  for preventing or promoting mammalian cell migration, preferably tumour
CC  cell migration in vitro or in vivo and to prevent tumour cell metastasis
CC  in a subject. An Ena/VASP activator or inhibitor is useful for promoting
CC  wound healing, preferably fibroblasts or nerve cells of a tissue type
CC  with the inhibitor to promote actin polymerisation and tissue formation
CC  on a scaffold. The inhibitor is also useful for preventing
CC  neurodegeneration such as in Alzheimer's disease, Down Syndrome,
CC  Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct
CC  trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia
CC  complex, progressive supranuclear palsy, progressive bulbar palsy,
CC  spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Rett's
CC  cerebellar degeneration, Tourettes syndrome, hypodyscaemia, hypoxia,
CC  Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP
CC  inhibitor is further useful for enhancing learning and memory in a
CC  subject having or at risk of developing a learning disorder such as
CC  Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile
CC  dementia, Korsakow's disorder and age-related memory loss. The inhibitor
CC  is administered in an amount for inhibiting the activity of Mena in a
CC  synapse. Ena/VASP activator is useful for disrupting learning and memory
CC  and the activator is administered in an amount to promote Ena/VASP
CC  protein-F655 interaction. Inducing the activity of Ena/VASP protein
CC  in immune or haematopoietic cells reduces the ability of the cells to
CC  migrate and this is useful for treating and preventing inflammatory
CC  disorders such as arthritis, allergy, gout, organ transplant,
CC  ulcerative colitis and ischaemic diseases and also for treating cancer
CC  metastasis. The present sequence represents the amino acid sequence
CC  of Ena/VASP homology (EVH) proline-rich motif #1.
XX
SQ  Sequence 5 AA;

Query Match      100.0%; Score 34; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 FPPPP 5
Db  1 fpppp 5

ULT 4
80051
AAR80051 standard; peptide; 4 AA.
XX
AC  AAR80051;
XX
DT  25-APR-1996 (first entry)
XX
DE  Peptidase substrate #5.
XX
KW  Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
KW  cerebral function.
XX
OS  Synthetic.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 1
FT  /label= OTHER
FT  /note= "hydroxyproline"
XX
PN  JP07227281-A.
XX
PD  29-AUG-1995.
XX
PF  15-FEB-1994; 94JP-0042027.
XX
PS  (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX  (NIHA-) NIPPON HAM KK.
XX
DR  WPI; 1995-331519/43.
XX
PT  140 kDa peptidase hydrolyses proline rich proteins - useful for
    prevention and treatment of diseases related to proline rich
    proteins and studies of cerebral functions
    Example 4; Page 6; 7pp; Japanese.
XX
CC  The sequences represented by AAR80046 and AAR80048-R80059 are substrates
CC  for the novel peptidase of the invention. The peptidase hydrolyses
CC  p-P-P, p-P-P, and p-P and recognises the proline at the second residue
CC  from the N-terminal of a peptide to release the N-terminal amino acid.
CC  The enzyme's activity is stimulated with MnCl2 and inhibited with the
CC  o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
CC  hydrolysis of proline containing physiologically active peptides,
CC  oligoproline and proline rich proteins in the living body, particularly
CC  in the brain of mammals. The peptidase is useful for the prevention and
CC  treatment of proline rich protein related diseases and study of cerebral
    functions.
XX
SQ  Sequence 4 AA;

Query Match      82.4%; Score 28; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 PPPP 5
    ||||
Db  1 pppp 4

RESULT 5
AAR80057
ID  AAR80057 standard; peptide; 4 AA.
XX
AC  AAR80057;
XX
DT  25-APR-1996 (first entry)
XX
DE  Peptidase substrate #11.
XX
KW  Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
KW  cerebral function.
XX
OS  Synthetic.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 2
FT  /label= OTHER
FT  /note= "hydroxyproline"
XX
PN  JP07227281-A.
XX
PD  29-AUG-1995.
XX
PF  15-FEB-1994; 94JP-0042027.
XX
PS  (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX  (NIHA-) NIPPON HAM KK.
XX
DR  WPI; 1995-331519/43.
XX
PT  140 kDa peptidase hydrolyses proline rich proteins - useful for
    prevention and treatment of diseases related to proline rich
    proteins and studies of cerebral functions
    Example 4; Page 6; 7pp; Japanese.
XX
CC  The sequences represented by AAR80046 and AAR80048-R80059 are substrates
CC  for the novel peptidase of the invention. The peptidase hydrolyses
CC  p-P-P, p-P-P, and p-P and recognises the proline at the second residue
CC  from the N-terminal of a peptide to release the N-terminal amino acid.
CC  The enzyme's activity is stimulated with MnCl2 and inhibited with the
CC  o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the
CC  hydrolysis of proline containing physiologically active peptides,
CC  oligoproline and proline rich proteins in the living body, particularly
CC  in the brain of mammals. The peptidase is useful for the prevention and
CC  treatment of proline rich protein related diseases and study of cerebral
    functions.
XX
SQ  Sequence 4 AA;

```

PT proteins and studies of cerebral functions

PS Example 4; Page 6; 7pp; Japanese.

XX The sequences represented by AAR80046 and AAR80048-R80059 are substrates  
CC for the novel peptidase of the invention. The peptidase hydrolyses  
CC P-P-P, P-P-P, and P-P and recognises the proline at the second residue  
CC from the N-terminal of a peptide to release the N-terminal amino acid.  
CC The enzyme's activity is stimulated with MnCl<sub>2</sub> and inhibited with  
CC o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the  
CC hydrolysis of proline containing physiologically active peptides,  
CC oligoproline and proline rich proteins in the living body, particularly  
CC in the brain of mammals. The peptidase is useful for the prevention and  
CC treatment of proline rich protein related diseases and study of cerebral  
CC functions.

XX Sequence 4 AA;

Query Match 82.4%; Score 28; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 pppp 5

Db 1 pppp 4

RESULT 6

AAR80048  
ID AAR80048 standard; peptide; 4 AA.

XX AAR80048;

XX 25-APR-1996 (first entry)

XX Peptidase substrate #2.

XX Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;  
KW cerebral function.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "optionally amidated"

XX JP07227281-A.

XX 29-AUG-1995.

XX 15-FEB-1994; 94JP-0042027.

XX 15-FEB-1994; 94JP-0042027.

XX (AGENCY) AGENCY OF IND SCI & TECHNOLOGY.

XX (NIHA-) NIPPON HAM KK.

XX WPI; 1995-331519/43.

XX 140 kDa peptidase hydrolyses proline rich proteins - useful for  
PT prevention and treatment of diseases related to proline rich  
PT proteins and studies of cerebral functions

PS Example 4; Page 6; 7pp; Japanese.

XX The sequences represented by AAR80046 and AAR80048-R80059 are substrates  
CC for the novel peptidase of the invention. The peptidase hydrolyses  
CC P-P-P, P-P-P, and P-P and recognises the proline at the second residue  
CC from the N-terminal of a peptide to release the N-terminal amino acid.  
CC The enzyme's activity is stimulated with MnCl<sub>2</sub> and inhibited with  
CC o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the  
CC hydrolysis of proline containing physiologically active peptides.

CC oligoproline and proline rich proteins in the living body, particularly  
CC in the brain of mammals. The peptidase is useful for the prevention and  
CC treatment of proline rich protein related diseases and study of cerebral  
CC functions.

XX Sequence 4 AA;

Query Match 82.4%; Score 28; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 pppp 5

Db 1 pppp 4

RESULT 7

AAW59261  
ID AAW59261 standard; peptide; 4 AA.

XX AAW59261;

XX 27-AUG-1998 (first entry)

XX BOP activated peptide #1.

XX Solid phase peptide synthesis; polymer; peptide array; cyclic;  
KW screening; detection; antibody; activity; dynorphin.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Activated by

FT benzotriazol-1-yloxytris-(dimethylamino)  
FT phosphonium hexafluorophosphate (BOP)"

FT Modified-site 4 /note= "C-terminal hydroxyl group"

XX US5770456-A.

XX 23-JUN-1998.

XX 13-MAY-1996; 96US-0647618.

XX 05-NOV-1992; 92US-0972007.

XX 07-JUN-1989; 89US-0362901.

XX 07-MAR-1990; 90US-0492462.

XX 06-DEC-1990; 90US-0624120.

XX 22-NOV-1991; 91US-0796727.

XX 06-DEC-1991; 91US-0805727.

XX 13-MAY-1996; 96US-0647618.

XX (AFFY-) AFFYMETRIX INC.

XX Holmes CP;

XX WPI; 1998-376811/32.

XX Cyclic nucleic acid and polypeptide arrays - useful for determining  
PT binding characteristics of a specific molecule to variations of the  
PT nucleic acid or polypeptide in the array

PS Example; Column 26; 35pp; English.

XX Peptides AAW59229-W59262 are used for the synthesis of diverse molecular  
CC sequences on substrates, using a procedure based on known solid phase  
CC synthesis principles. Initially a first 'monomer' (nucleotide or amino  
CC acid) is bound to synthesis sites (through a tether molecule). Using a  
CC series of masking steps, a second monomer is added to the first and also  
CC to new synthesis sites (i.e. bound to the carrier as well as in addition  
CC to the first monomer). This is repeated to obtain a series of polymers

CC of differing length, but essentially comprising the same sequence. Using  
 CC different masking strategies, the synthesis steps are repeated,  
 CC resulting in the same sequence but starting at a different position. By  
 CC cyclising the polymer, a range of exposed portions, all based on the same  
 CC sequence are possible. This array can then be used to screen for  
 CC biological activity of e.g. antibodies, oligonucleotides, cells,  
 CC receptors etc. for the sequences they bind to, by detecting at which  
 CC position on the array they are at (e.g. by having the compound being  
 CC tested attached to a fluorescent marker or other detection molecule). The  
 CC array can be used to quickly screen many possible binding sites for a  
 CC molecule, by knowing at positions on the array (and therefore the  
 CC sequence) e.g. an antibody will bind to.  
 XX  
 SQ Sequence 4 AA;

Query Match 82.4%; Score 28; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 PPPP 5  
 ||||  
 Db 1 PPPP 4

RESULT 8  
 AAR97694  
 ID AAR97694 standard; Peptide; 5 AA.

XX AC AAR97694;

XX DT 30-AUG-1996 (first entry)

XX DE WW domain ligand PY motif.

XX KW WW domain; signal transduction; diagnosis; gene therapy;

XX KW Yes proto-oncogene associated protein; YAP; ligand; WBP-1;

XX KW WBP-2.

XX OS Mus sp.

XX PN WO9617061-Al.

XX PD 06-JUN-1996.

XX PF 30-NOV-1995; 95WO-US15512.

XX PR 07-JUN-1995; 95US-0476509.

XX PR 01-DEC-1994; 94US-0348518.

XX PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.  
 XX PA (UYRQ ) UNIV ROCKEFELLER.

XX PI Bork P, Chen H, Sudol M;

XX DR WPI; 1996-286829/29.

XX PT DNA encoding Yes proto-oncogene associated protein - used to  
 PT modulate intracellular signal transduction e.g. for treatment of  
 PT muscular dystrophy

XX PS Claim 51; Page 100; 126pp; English.

XX CC WW domain ligands WBP-1 and WBP-2 have an invariant proline-rich  
 CC region (AAR97694) termed the PY motif. WBP-1 (AAR97695) and WBP-2  
 CC (AAR97696) are ligands for the WW signalling domain of human Yes  
 CC proto-oncogene associated protein, YAP (AAR97670). The PY motif  
 CC is involved in binding the WBP2 to the WW domain. It does not  
 CC conform to the consensus of SH3-binding proline-rich domains,  
 CC but appears to require a different consensus (AAR97693) sequence for  
 CC binding. Residues surrounding the PY motif may impart specificity  
 CC for a particular WW domain. Mutagenesis of any of the residues  
 CC of the motif (see AAR97698-700 and AAR98322-23) abolished or

CC reduced binding to the WW domain.

SQ Sequence 5 AA;

Query Match 82.4%; Score 28; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5

||||

Db 1 PPPP 4

RESULT 9

AAW37648  
 ID AAW37648 standard; Peptide; 5 AA.

XX AC AAW37648;

XX DT 23-APR-1998 (first entry)

XX DE PPPPY motif found in peptides that bind WW domains.

XX KW Peptide recognition unit; WW domain; cell signalling; growth regulation;

XX KW cytoskeleton organisation; targeted drug screening; modulator;

XX KW WW domain interaction; YAP protein; dystrophin.

XX OS Synthetic.

XX PN WO9737223-Al.

XX PD 09-OCT-1997.

XX PF 03-APR-1997; 97WO-US05547.

XX PR 03-APR-1996; 96US-0630916.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Fowlkes DM, Kay BK, Pirozzi G;

XX DR WPI; 1997-503234/46.

XX PT Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are  
 PT useful in targetted drug selection

XX PS Disclosure; Page 6; 220pp; English.

XX CC The present mtif is found in the proline rich regions of WBP-1 and WBP-2  
 CC proteins. Peptides containing this residue have been shown to bind the  
 CC YAP WW domain, but not the WW domain from dystrophin or to a panel of  
 CC SH3 domains. The WW domain is a small functional domain. Its name  
 CC is derived from the observation that two tryptophan residues, one in the  
 CC amino terminal portion of the WW domain and one in the carboxyl terminal  
 CC portion, are conserved. Most proteins containing WW domains have a  
 CC function involving cell signalling and growth regulation or the  
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain are  
 CC identified by treating a multivalent recognition unit complex that has  
 CC selective binding affinity for a WW domain, with many polypeptides and  
 CC identifying those with selective affinity for the complex. Proteins  
 CC containing WW domains are used for targeted drug screening, i.e. to  
 CC identify potential modulators of specific WW domain interactions.

SQ Sequence 5 AA;

Query Match 82.4%; Score 28; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 pppp 5  
 Db 1 pppp 4

RESULT 10  
 AAW65842  
 ID AAW65842 standard; peptide; 5 AA.  
 XX  
 AC AAW65842;  
 XX  
 DT 19-OCT-1998 (first entry)  
 XX  
 DE Peptide #67 from pentapeptide combinatorial library #3.  
 XX  
 KW polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPT;  
 KW ptiptydyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;  
 KW neuronal damage; combinatorial library.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Misc-difference 5  
 FT /note= "equimolar mixtures of 18 amino acids (all  
 FT naturally occurring amino acids except tryptophan and  
 FT cysteine), C-terminal amide"  
 XX  
 PN WO9825950-Al.  
 XX  
 PD 18-JUN-1998.  
 XX  
 PF 08-DEC-1997; 97WO-US23102.  
 XX  
 PR 09-DEC-1996; 96US-0761902.  
 XX  
 PA (GUIL-) GUILFORD PHARM INC.  
 XX  
 PI Hamilton GS, Steiner JP, Wei L;  
 XX  
 DR WPI; 1998-348444/30.  
 XX  
 XX Effecting neuronal activity in mammals - by administering tetra-  
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,  
 PT useful in treatment of neuronal damage or degeneration disorders  
 XX  
 PS Example 2; Page 31; 70pp; English.  
 XX  
 CC The invention relates to neurotrophic low molecular weight, small  
 CC molecule peptidic cyclophilin inhibitor compounds having an affinity for  
 CC cyclophilin-type immunophilins, and their use as inhibitors of the  
 CC enzyme activity associated with immunophilin proteins, particularly  
 CC peptidyl-prolyl isomerase, or rotamase, enzyme activity. Tetrapeptide  
 CC and pentapeptide combinatorial libraries were used to map the substrate  
 CC specificity of the enzyme cyclophilin. Pools of tetrapeptide and  
 CC pentapeptide substrates were generated and their potencies in binding to  
 CC cyclophilin A were evaluated by examining the inhibition of peptidyl-  
 CC prolyl isomerase activity. Positional scanning technique was used to  
 CC determine the optimal amino acid(s) for each position of the tetra- or  
 CC penta-peptide. The present sequence represents one of the peptide pools  
 CC used.  
 XX  
 SQ Sequence 5 AA;

Query Match 82.4%; Score 28; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 pppp 5  
 Db 1 pppp 4

RESULT 11  
 AAW47014  
 ID AAW47014 standard; Peptide; 5 AA.  
 XX  
 AC AAW47014;  
 XX  
 DT 03-AUG-1998 (first entry)  
 XX  
 DE Daucus carota SERK peptide.  
 XX  
 KW receptor kinase; apomixis; apomictic; seeds; production; embryos;  
 KW plant breeding.  
 XX  
 OS Daucus carota.  
 XX  
 PN WO9743427-Al.  
 XX  
 PD 20-NOV-1997.  
 XX  
 PF 13-MAY-1997; 97WO-EP02443.  
 XX  
 PR 14-MAY-1996; 96GB-0010044.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;  
 XX  
 DR WPI; 1998-086529/08.  
 XX  
 PT Production of apomictic seeds - useful in plant breeding  
 XX  
 PS Disclosure; Page 61; 123pp; English.  
 XX

The sequence is that of a peptide fragment of SERK, a putative receptor kinase. SERK may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

SQ Sequence 5 AA;

Query Match 82.4%; Score 28; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 pppp 5  
 Db 1 pppp 5

RESULT 12  
 AAW37156  
 ID AAW37156 standard; Peptide; 5 AA.  
 XX  
 AC AAW37156;  
 XX



DT 06-JUL-1998 (first entry)  
XX Mammalian Ena (Mena) and Evi motif.  
DE  
XX Mena protein; mammalian Ena; Enabled; Evi protein; cytoskeleton;  
KW cell morphology; cell adhesion; cell differentiation; cell growth;  
KW cell motility; mouse.  
XX  
OS Mus musculus.  
XX  
XX WO9801755-A1.  
XX  
XX 15-JAN-1998.  
XX  
XX 03-JUL-1997; 97WO-US11669.  
XX  
XX 05-JUL-1996; 96US-0675815.  
XX  
XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
XX  
XX Gertler FB, Niebuhr K, Soriano P, Wehland J;  
XX WPI; 1998-101197/09.  
XX  
XX Detection of modulators of Mena and Ena-VASP-like genes and proteins  
PT - used in control of cytoskeletal dynamic events in normal and  
PT abnormal cell morphology, adhesion, motility, growth and  
PT differentiation  
XX  
XX Example 1; Page 37; 77pp; English.  
XX  
XX This peptide motif is present twice in novel mouse Mena (mammalian  
CC Ena) protein (see AAW37148) and once in novel mouse Ena-VASP-like  
CC Evi protein (see AAW37149). It mediates binding to the actin-monomer  
CC sequestering protein profilin. The invention relates to disclosed  
CC Mena and Evi genes (see AAV02966-98) and proteins (see AAW37148-53),  
CC and a variety of methods and compositions used for screening,  
CC isolating and characterising endogenous and exogenous factors,  
CC drugs and therapeutic agents useful to evaluate and/or control  
CC cytoskeletal dynamic events involved in normal and abnormal cell  
CC morphology, adhesion, motility, growth and/or differentiation.  
XX  
SQ Sequence 5 AA;  
  
Query Match 82.4%; Score 28; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPPP 5  
DB 2 PPPP 5  
  
RESULT 13  
AAW98982  
ID AAW98982 standard; peptide; 5 AA.  
XX  
XX AAW98982;  
XX  
XX 11-MAY-1999 (first entry)  
XX  
XX FAM-(Pro)4-Lys(epsilon-TMR) peptide.  
XX  
XX Energy transfer; DNA base sequencing; reporter; donor; acceptor;  
KW terminator; chain terminator method.  
XX  
XX Synthetic.  
OS  
XX WO9902544-A1.  
XX  
XX 21-JAN-1999.  
PD

XX 10-JUL-1998; 98WO-JP03093.  
PF  
XX 11-JUL-1997; 97JP-0186886.  
PR  
XX (RIKA) INST PHYSICAL & CHEM RES.  
PA (WAKP) WAKO PURE CHEM IND LTD.  
XX  
XX Hayashizaki Y, Tanaka T;  
PI  
XX WPI; 1999-120768/10.  
DR  
XX New nucleotide derivatives having energy transfer function - contain  
XX reporters to serve as donor and acceptor, useful in chain  
PT termination DNA base sequencing  
PT  
XX Example; Page 41; 75pp; Japanese.  
PS  
XX The present invention describes nucleotide compounds of formula (I):  
CC Q-V-CO-R1(NH-W2)-NH(CO-CHR2-NR3)m-W1 (I) Q = mono or oligonucleotide;  
CC V = C triple bond C-(CH2)nNH or CH-CH(CH2)n2NH; n1, n2, m = integer;  
CC R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring;  
CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase  
CC and a mono or oligonucleotide compound (I') as initiator in a chain  
CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate  
CC group; and (ii) two reporters capable of serving as a donor and an  
CC acceptor in energy transfer. (I') including (I) have improved uptake  
CC efficiency by RNA polymerases and can so be used with RNA polymerases  
CC as terminators in DNA base sequencing methods. The present sequence  
CC represents a peptide used in an example from the present invention.  
XX  
SQ Sequence 5 AA;  
  
Query Match 82.4%; Score 28; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPPP 5  
DB 1 PPPP 4  
  
RESULT 14  
AAU09141  
ID AAU09141 standard; peptide; 5 AA.  
XX  
XX AAU09141;  
XX  
XX 19-DEC-2001 (first entry)  
DT  
XX Ena/VASP homology (EVH) proline-rich motif #2.  
XX  
XX Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
KW cancer; ischaemia.  
XX  
XX Listeria monocytogenes.  
OS  
XX WO200174853-A2.  
XX  
XX 11-OCT-2001.  
PD  
XX 30-MAR-2001; 2001WO-US10249.  
XX  
XX 03-APR-2000; 2000US-194564P.  
XX



XX 14-DEC-1999; 99US-0170550.  
PR 11-APR-2000; 2000US-0196266.  
XX (GENO-) GENOVO INC.  
PA Himes VB, Rasty S, Peluso RW;  
XX WPI; 2001-475764/51.  
DR N-PSDB; AAH42482.  
XX New nucleic acids for creating complementing cell lines that enable  
PT production of high titer adenovirus vectors, comprises a sequence of a  
PT polynucleotide which is not a naturally-occurring adenoviral nucleotide  
PT sequence -  
XX  
PS Example 1; Page 96; 104pp; English.  
XX The specification describes a nucleic acid molecule, comprising a  
CC polynucleotide encoding 5 contiguous amino acids of a naturally-occurring  
adenovirus (Ad) polypeptide, where the polynucleotide is not a  
naturally-occurring adenoviral nucleotide sequence and is useful for  
creating complementing cell lines that enable the efficient production  
of high titer Ad vectors. The nucleic acid molecule is useful for  
creating Ad-complementary cell lines which are useful for high yield  
production of recombinant replication-incompetent Ad vectors, in the  
absence of detectable replication competent Ad. The adenoviruses  
free of contamination with RCA are suitable for preclinical and  
clinical use. El-deleted viruses are suitable for applications in which  
transient transgene expression is therapeutic (e.g. p53 gene transfer  
in cancer, beta-interferon gene transfer in cancer, platelet derived  
growth factor (PDGF) gene transfer in wound healing, and vascular  
endothelial growth factor (VEGF) gene transfer in vascular diseases of  
the heart and limbs). The present sequence encodes a human Ad5 Elb 8.3  
kDa protein. It is used to construct an E1 complementation element, for  
use in the course of the invention.  
XX  
SQ Sequence 5 AA;  
  
Query Match 82.4%; Score 28; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 PPPP 5  
Db 2 PPPP 5  
  
ULT 17  
AAB72257  
ID AAB72257 standard; peptide; 5 AA.  
XX AC AAB72257;  
XX 14-MAY-2001 (first entry)  
XX Colostrinin derived cytokine inducing peptide SEQ ID 12.  
XX Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX Synthetic.  
XX WO200111937-A2.  
XX 22-FEB-2001.  
XX 17-AUG-2000; 2000WO-US22818.  
XX 17-AUG-1999; 99US-0149311.  
PR

XX (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2001-202804/20.  
XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX Claim 1; Page 34; 50pp; English.  
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.  
XX  
SQ Sequence 5 AA;  
  
Query Match 79.4%; Score 27; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FPPP 4  
Db 1 fppp 4  
  
RESULT 18  
AAB72510  
ID AAB72510 standard; Peptide; 5 AA.  
XX AC AAB72510;  
XX 09-MAY-2001 (first entry)  
XX Colostrinin peptide #11.  
XX Dermatological; oxidative stress regulator; colostrinin.  
XX Unidentified.  
XX WO200112650-A2.  
XX 22-FEB-2001.  
XX 17-AUG-2000; 2000WO-US22665.  
XX 17-AUG-1999; 99US-0149310.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.  
XX Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX Claim 6; Page 25; 48pp; English.  
XX

CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 5 AA;

Query Match 79.4%; Score 27; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 fppp 4  
| | | |  
Db 1 fppp 4

RESULT 19  
AAB72542  
ID AAB72542 standard; Peptide; 5 AA.

XX AC AAB72542;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #11.  
XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
XX KW colostrum.  
XX OS Unidentified.  
XX PN WO200112651-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22774.  
XX PR 17-AUG-1999; 99US-0149633.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Boldogh I;  
XX DR WPI; 2001-226545/23.

XX Use of colostrinin, its constituent peptide or analog as a neural cell  
XX regulator, for promoting neural cell differentiation and treating  
XX damaged neural cells in a patient -  
XX  
XX Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell  
XX differentiation and treating damaged neural cells, using colostrinin and  
XX colostrinin constituent peptides (e.g. the present peptide) as a neural  
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
SQ Sequence 5 AA;

Query Match 79.4%; Score 27; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 fppp 4  
| | | |  
Db 1 fppp 4

RESULT 20

AAB59320  
ID AAB59320 standard; Peptide; 5 AA.  
XX AC AAB59320;  
XX DT 21-MAR-2001 (first entry)  
XX DE Ewe colostrinin peptide fragment B-5.  
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX OS Ovis sp.  
XX PN WO200075173-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-GB02128.  
XX PR 02-JUN-1999; 99GB-0012852.  
XX PA (REGG-) REGEN THERAPEUTICS PLC.  
XX PI Georgiades JA;  
XX DR WPI; 2001-071058/08.  
XX PT Peptides having an N-terminal amino acid sequence isolated from  
XX PT colostrinin for treating e.g. disorders of the central nervous system  
XX PT and immune system, viral and bacterial infections, and diseases  
XX PT characterized by amyloid plaques -  
XX PS Claim 7; Page 27; 63pp; English.  
XX CC The present invention provides the sequences of a number of peptides  
XX CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
XX CC fragment of colostrum. These peptides can be used in the treatment of  
XX CC central nervous system disorders such as senile dementia, Parkinson's  
XX CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
XX CC disorders such as bacterial and viral infections, to improve the  
XX CC development of a child's immune system, as a dietary supplement, and to  
XX CC promote the dissolution of beta-amyloid plaques.

SQ Sequence 5 AA;

Query Match 79.4%; Score 27; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 fppp 4  
| | | |  
Db 1 fppp 4

RESULT 21  
AAB91724  
ID AAB91724 standard; Peptide; 4 AA.

XX AC AAB91724;  
XX DT 22-JUN-2001 (first entry)  
XX DE Opioid peptide SEQ ID NO:900.  
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
XX KW blood component; modification; succinimidy1; maleimido group; amino;  
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX OS Homo sapiens.  
XX OS Synthetic.



XX Prolyl endopeptidase inhibitor for treating dementia - are  
PT prepared by hydrolysis of corn protein  
XX  
XX Claim 1; Page 2; 8pp; Japanese.  
XX  
CC This peptide is one of 10 claimed peptides having prolyl  
CC endopeptidase inhibitory activity; the peptide is expected to be of  
CC use for the prophylaxis and treatment of dementia. The peptide can  
CC be prepared by hydrolysis of gamma-zein from corn or by standard  
CC peptide synthesis.

XX Sequence 4 AA;  
SQ

Query Match 61.8%; Score 21; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XY 2 PPP 4  
b IIII  
1 ppp 3

RESULT 24  
AAR80046  
ID AAR80046 standard; peptide; 4 AA.  
XX AC AAR80046;  
XX XX  
DT 25-APR-1996 (first entry)  
XX DE Peptidease substrate #1.  
XX KW Peptidease; o-phenanthroline; 2-mercaptoethanol; oligoproline;  
KW cerebral function.  
XX OS Synthetic.  
XX JP07227281-A.  
PN 29-AUG-1995.  
XX 15-FEB-1994; 94JP-0042027.  
PF 15-FEB-1994; 94JP-0042027.  
PR (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
PA (NIHA-) NIPPON HAM KK.  
X WPI; 1995-331519/43.  
DR  
XX 140 kDa peptidase hydrolyses proline rich proteins - useful for  
PT prevention and treatment of diseases related to proline rich  
PT proteins and studies of cerebral functions  
XX Example 4; Page 6; 7pp; Japanese.  
XX The sequences represented by AAR80046 and AAR80048-R80059 are substrates  
XX for the novel peptidase of the invention. The peptidase hydrolyses  
XX P-P-P, P-P-P, and P-P and recognises the proline at the second residue  
XX from the N-terminal of a peptide to release the N-terminal amino acid.  
XX The enzyme's activity is stimulated with MnCl<sub>2</sub> and inhibited with  
XX o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the  
XX hydrolysis of proline containing physiologically active peptides,  
XX oligoprolines and proline rich proteins in the living body, particularly  
XX in the brain of mammals. The peptidase is useful for the prevention and  
XX treatment of proline rich protein related diseases and study of cerebral  
CX functions.  
XX Sequence 4 AA;  
SQ

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10/10/2002

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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:14:48 ; Search time 15.94 Seconds  
(without alignments)  
7.662 Million cell updates/sec

Title: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 17877

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	82.4	4	1	US-07-972-007-33
2	28	82.4	4	1	US-08-351-058A-1
3	28	82.4	4	1	US-08-647-618-33
4	28	82.4	4	2	US-08-358-556A-21
5	28	82.4	4	5	PCT-US92-09964-1
6	28	82.4	5	1	US-08-351-058A-5
7	28	82.4	5	1	US-08-477-509B-9
8	28	82.4	5	2	US-08-358-556A-23
9	28	82.4	5	3	US-08-630-916A-3
10	28	82.4	5	3	US-08-482-085B-9
11	28	82.4	5	3	US-08-476-509B-38
12	28	82.4	5	4	US-09-444-791A-9
13	28	82.4	5	5	PCT-US92-09964-5
14	21	61.8	4	1	US-08-477-509B-106
15	21	61.8	4	3	US-08-482-085B-106
16	21	61.8	4	4	US-09-444-791A-106
17	21	61.8	5	2	US-08-666-473-6
18	21	61.8	5	2	US-08-666-473-9
19	21	61.8	5	2	US-08-666-473-10
20	21	61.8	5	2	US-08-340-283-3
21	21	61.8	5	2	US-08-340-283-4
22	21	61.8	5	2	US-08-967-508-12
23	21	61.8	5	2	US-08-967-508-13
24	21	61.8	5	3	US-08-967-506-12
25	21	61.8	5	3	US-08-967-506-13
26	21	61.8	5	5	PCT-US94-02552-12
27	21	61.8	5	5	PCT-US94-02552-13

RESULT 1  
US-07-972-007-33  
; Sequence 33, Application US/07972007  
; Patent No. 5527681  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; TITLE OF INVENTION: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/972.007  
; FILING DATE: 19921105  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5527681viel, Vernon A.  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 11509-57-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-972-007-33

#### ALIGNMENTS

Sequence 3, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 18, Appli  
Sequence 40, Appli  
Sequence 12, Appli  
Sequence 8, Appli  
Sequence 20, Appli  
Sequence 71, Appli  
Sequence 13, Appli  
Sequence 9, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 3, Appli  
Patent No. 5425936  
Patent No. 5433940  
Sequence 2, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Patent No. 5196404

Query Match 82.4%; Score 28; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
||||  
Db 1 PPPP 4

## RESULT 2

US-08-351-058A-1  
; Sequence 1, Application US/08351058A  
; Patent No. 5550215  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,058A  
; FILING DATE: 28-NOV-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,940  
; FILING DATE: 19-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-351-058A-1

Query Match 82.4%; Score 28; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
||||  
Db 1 PPPP 4

## RESULT 3

US-08-647-618-33  
; Sequence 33, Application US/08647618  
; Patent No. 5770456  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; MOLECULE TYPE: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/647,618  
; FILING DATE: 13-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/972,007  
; FILING DATE: 05-NOV-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/805,727  
; FILING DATE: 06-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/624,120  
; FILING DATE: 06-DEC-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/492,462  
; FILING DATE: 07-MAR-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/362,901  
; FILING DATE: 07-JUN-1989  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Matthew B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 16528J-000141US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-647-618-33

Query Match 82.4%; Score 28; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
||||  
Db 1 PPPP 4

## RESULT 4

US-08-358-556A-21  
; Sequence 21, Application US/08358556A  
; Patent No. 5869643  
; GENERAL INFORMATION:  
; APPLICANT: Chatelein, Francois  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: a Solid Support and Apparatus Permitting its

;; TITLE OF INVENTION: Implementation  
;; NUMBER OF SEQUENCES: 31  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jacobson, Price, Holman & Stern  
;; STREET: 400 Seventh St. N.W.  
;; CITY: Washington D.C  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/358,556A  
;; FILING DATE: 14-DEC-1994  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 9315164  
;; FILING DATE: 16-DEC-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)638-6666  
;; TELEFAX: (202) 393-3350  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-358-556A-21

Query Match 82.4%; Score 28; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PPPP 5  
Db 1 PPPP 4

RESULT 5  
-US92-09964-1  
Sequence 1, Application PC/TUS9209964  
GENERAL INFORMATION:  
;; APPLICANT: Holmes, Christopher P.  
;; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US92/09964  
;; FILING DATE: 19921119  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/796,727  
;; FILING DATE: 22-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 11509-51-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; PCT-US92-09964-1

Query Match 82.4%; Score 28; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PPPP 5  
Db 1 PPPP 4

RESULT 6  
US-08-351-058A-5  
Sequence 5, Application US/08351058A  
Patent No. 5550215  
GENERAL INFORMATION:  
;; APPLICANT: Holmes, Christopher P.  
;; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Burns, Doane, Swecker & Mathis  
;; STREET: P.O. Box 1404  
;; CITY: Alexandria  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22313-1404  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/351,058A  
;; FILING DATE: 28-NOV-1994  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/978,940  
;; FILING DATE: 19-NOV-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/796,727  
;; FILING DATE: 22-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Swiss, Gerald F.  
;; REGISTRATION NUMBER: 30,113  
;; REFERENCE/DOCKET NUMBER: 000324-015  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-854-7400  
;; TELEFAX: 415-854-8275  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-351-058A-5

Query Match 82.4%; Score 28; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 7

US-08-477-509B-9  
; Sequence 9, Application US/08477509B  
; Patent No. 5770697  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W  
; APPLICANT: Dorman, Mary A  
; TITLE OF INVENTION: No 5770697el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,509B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Irecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-509B-9

Query Match 82.4%; Score 28; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 8

US-08-358-556A-23  
; Sequence 23, Application US/08358556A  
; Patent No. 5869643  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its  
; TITLE OF INVENTION: Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,556A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9315164  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-358-556A-23

Query Match 82.4%; Score 28; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 9

US-08-630-916A-3  
; Sequence 3, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States

ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-3

Query Match 82.4%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Oy 2 PPPP 5  
Db 1 PPPP 4

RESULT 10  
US-08-482-085B-9  
Sequence 9, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482.085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-9

Query Match 82.4%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Oy 2 PPPP 5  
Db 2 PPPP 5

RESULT 11  
US-08-476-509B-38  
Sequence 38, Application US/08476509B  
Patent No. 6034212  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,509B  
FILING DATE: 01-DEC-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-476-509B-38

Query Match 82.4%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
Db 1 PPPP 4

## RESULT 12

US-09-444-791A-9  
; Sequence 9, Application US/09444791A  
; Patent No. 6355776

## GENERAL INFORMATION:

APPLICANT: Ferrari, Franco A.  
Richardson, Charles  
Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.

TITLE OF INVENTION: NO. 6355776el Peptides Comprising Repetitive

UNITS OF AMINO ACIDS AND DNA SEQUENCES ENCODING THE SAME

## NUMBER OF SEQUENCES: 117

## CORRESPONDENCE ADDRESS:

ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,791A

FILING DATE: 22-NOV-1999

CLASSIFICATION: <unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,085

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

## ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-11/RPT/BTC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

## INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-444-791A-9

Query Match 82.4%; Score 28; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
Db 2 PPPP 5

## RESULT 13

PCT-US92-09964-5

; Sequence 5, Application PC/TUS9209964

GENERAL INFORMATION:

APPLICANT: Holmes, Christopher P.

TITLE OF INVENTION: Polymer Reversal on Solid Surfaces

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09964

FILING DATE: 19921119

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,727

FILING DATE: 22-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11509-51-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: peptide

PCT-US92-09964-5

Query Match 82.4%; Score 28; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
Db 2 PPPP 5

## RESULT 14

US-08-477-509B-106

; Sequence 106, Application US/08477509B

Patent No. 5770697

GENERAL INFORMATION:

APPLICANT: Ferrari, Franco A

APPLICANT: Cappello, Joseph

APPLICANT: Crissman, John W

APPLICANT: Dorman, Mary A

;; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
;; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
;; NUMBER OF SEQUENCES: 112  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
;; STREET: Four Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/477,509B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/175,155  
;; FILING DATE: 29-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/053,049  
;; FILING DATE: 04-NOV-1986  
;; FILING DATE: 22-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/114,618  
;; FILING DATE: 29-OCT-1987  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 06/927,258  
;; FILING DATE: 04-NOV-1986  
;; FILING DATE: 22-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/114,618  
;; FILING DATE: 29-OCT-1987  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trecartin, Richard F.  
;; REGISTRATION NUMBER: 31,801  
;; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-398-3249  
;; TELEFAX: 415-398-3249  
;; INFORMATION FOR SEQ ID NO: 106:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-477-509B-106

Query Match 61.8%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPP 4  
Db 2 PPP 4

RESULT 15  
US-08-482-085B-106  
; Sequence 106, Application US/08482085B  
; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
;; STREET: Four Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,085B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 06/927,258  
;; FILING DATE: 04-NOV-1986  
;; FILING DATE: 22-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/114,618  
;; FILING DATE: 29-OCT-1987  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/053,049  
;; FILING DATE: 22-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/175,155  
;; FILING DATE: 29-DEC-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trecartin, Richard F.  
;; REGISTRATION NUMBER: 31,801  
;; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-781-1989  
;; TELEFAX: 415-398-3249  
;; INFORMATION FOR SEQ ID NO: 106:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-482-085B-106

Query Match 61.8%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPP 4  
Db 2 PPP 4

RESULT 16  
US-09-444-791A-106  
; Sequence 106, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California

COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 19-SEP-1996  
CLASSIFICATION: 435  
APPLICATION NUMBER: US/08/666,473  
PRIORITY APPLICATION DATA:  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: WO PCT/JP95/02238  
PRIORITY APPLICATION DATA:  
FILING DATE: 09-FEB-1995  
APPLICATION NUMBER: JP 7-22101  
PRIORITY APPLICATION DATA:  
FILING DATE: 01-NOV-1994  
APPLICATION NUMBER: JP 6-269111  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16887/837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-666-473-6

Query Match 61.8%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 2 ppp 4  
Db 3 ppp 5

RESULT 17  
US-08-666-473-6  
; Sequence 6, Application US/08666473  
; Patent No. 5843713  
; GENERAL INFORMATION:  
; APPLICANT: YOSHIDA, Aruto  
; APPLICANT: TAKEUCHI, Makoto  
; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19-SEP-1996  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US/08/666,473  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 01-NOV-1995  
; APPLICATION NUMBER: WO PCT/JP95/02238  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 09-FEB-1995  
; APPLICATION NUMBER: JP 7-22101  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 01-NOV-1994  
; APPLICATION NUMBER: JP 6-269111  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RPT/BTC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..4  
; OTHER INFORMATION: /note= "X = any amino acid"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
US-09-444-791A-106

Query Match 61.8%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 2 ppp 4  
Db 3 ppp 4

RESULT 17  
US-08-666-473-6  
; Sequence 6, Application US/08666473  
; Patent No. 5843713  
; GENERAL INFORMATION:  
; APPLICANT: YOSHIDA, Aruto  
; APPLICANT: TAKEUCHI, Makoto  
; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 19-SEP-1996  
CLASSIFICATION: 435  
APPLICATION NUMBER: US/08/666,473  
PRIORITY APPLICATION DATA:  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: WO PCT/JP95/02238  
PRIORITY APPLICATION DATA:  
FILING DATE: 09-FEB-1995  
APPLICATION NUMBER: JP 7-22101  
PRIORITY APPLICATION DATA:  
FILING DATE: 01-NOV-1994  
APPLICATION NUMBER: JP 6-269111  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16887/837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-666-473-6

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 2 ppp 4  
Db 3 ppp 5

RESULT 18  
US-08-666-473-9  
; Sequence 9, Application US/08666473  
; Patent No. 5843713  
; GENERAL INFORMATION:  
; APPLICANT: YOSHIDA, Aruto  
; APPLICANT: TAKEUCHI, Makoto  
; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19-SEP-1996  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US/08/666,473  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 01-NOV-1995  
; APPLICATION NUMBER: WO PCT/JP95/02238  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 09-FEB-1995  
; APPLICATION NUMBER: JP 7-22101  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 01-NOV-1994  
; APPLICATION NUMBER: JP 6-269111  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16887/837  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-666-473-6



APPLICATION NUMBER: JP 7-22101  
FILING DATE: 09-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-269111  
FILING DATE: 01-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16887/837  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
8-666-473-9

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 3 PPP 5

RESULT 19  
US-08-666-473-10  
Sequence 10, Application US/08666473  
Patent No. 5843713  
GENERAL INFORMATION:  
APPLICANT: YOSHIDA, Aruto  
APPLICANT: TAKEUCHI, Makoto  
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/666.473  
FILING DATE: 19-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP95/02238  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION NUMBER: JP 7-22101  
FILING DATE: 09-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-269111  
FILING DATE: 01-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16887/837  
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-666-473-10

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 3 PPP 5

RESULT 20  
US-08-340-283-3  
Sequence 3, Application US/08340283  
Patent No. 5861318  
GENERAL INFORMATION:  
APPLICANT: Elhammer, Ake P.  
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR  
TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY  
NUMBER OF SEQUENCES: 205  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law  
ADDRESSEE: (1920-32-1)  
STREET: 301 Henrietta Street  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: U.S.A.  
ZIP: 49001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,283  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Wootton, Thomas A.  
REGISTRATION NUMBER: 35,004  
REFERENCE/DOCKET NUMBER: 4828  
TELEPHONE: (616) 385-7914  
TELEFAX: (616) 385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-340-283-3

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||

Db 3 PPP 5

## RESULT 21

US-08-340-283-4  
; Sequence 4, Application US/08340283  
; Patent No. 5961318  
; GENERAL INFORMATION:  
; APPLICANT: Elhammer, Ake P.  
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR  
; N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY  
; NUMBER OF SEQUENCES: 205  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellectual. Prop. Law  
; ADDRESS: (1920-32-1)  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: U.S.A.  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/340,283  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wootton, Thomas A.  
; REGISTRATION NUMBER: 35,004  
; REFERENCE/DOCKET NUMBER: 4828  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (616) 385-7914  
; TELEFAX: (616) 385-6897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; US-08-340-283-4

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 3 PPP 5

## RESULT 22

US-08-967-508-12  
; Sequence 12, Application US/08967508  
; Patent No. 5910570  
; GENERAL INFORMATION:  
; APPLICANT: The Upjohn Company  
; APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.  
; TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAC:  
; N-ACETYL GALACTOSAMINYLTRANSFERASE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company, Intellectual  
; ADDRESS: Property Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,508  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 08/602,830  
; FILING DATE: 13 No. 5910570ember 1995

CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,508  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,830  
; FILING DATE: 13 No. 5910570ember 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Darnley Jr., James D.  
; REGISTRATION NUMBER: 33,673  
; REFERENCE/DOCKET NUMBER: 4755.P CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-833-2210  
; TELEFAX: 616-833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-967-508-12

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 3 PPP 5

## RESULT 23

US-08-967-508-13  
; Sequence 13, Application US/08967508  
; Patent No. 5910570  
; GENERAL INFORMATION:  
; APPLICANT: The Upjohn Company  
; APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.  
; TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAC:  
; N-ACETYL GALACTOSAMINYLTRANSFERASE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company, Intellectual  
; ADDRESS: Property Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,508  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 08/602,830  
; FILING DATE: 13 No. 5910570ember 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Darnley Jr., James D.  
REGISTRATION NUMBER: 33,673  
REFERENCE/DOCKET NUMBER: 4755.P CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616-833-2210  
TELEFAX: 616-833-8897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-967-508-13

Query Match 61.8%; Score 21; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 3 PPP 5

RESULT 24  
US-08-967-506-12  
; Sequence 12, Application US/08967506  
; Patent No. 6096512  
; GENERAL INFORMATION:  
; APPLICANT: The Upjohn Company  
; APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.  
; TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAC:  
; TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company, Intellectual  
; ADDRESSEE: Property Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,506  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,830  
; FILING DATE: 13 No. 6096512ember 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Darnley Jr., James D.  
; REGISTRATION NUMBER: 33,673  
; REFERENCE/DOCKET NUMBER: 4755.P CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-833-2210  
; TELEFAX: 616-833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-967-506-12

Query Match 61.8%; Score 21; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
DB 3 PPP 5

RESULT 25  
US-08-967-506-13  
; Sequence 13, Application US/08967506  
; Patent No. 6096512  
; GENERAL INFORMATION:  
; APPLICANT: The Upjohn Company  
; APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.  
; TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAC:  
; TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Company, Intellectual  
; ADDRESSEE: Property Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/967,506  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,830  
; FILING DATE: 13 No. 6096512ember 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Darnley Jr., James D.  
; REGISTRATION NUMBER: 33,673  
; REFERENCE/DOCKET NUMBER: 4755.P CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-833-2210  
; TELEFAX: 616-833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-967-506-13

Query Match 61.8%; Score 21; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 3 PPP 5

Search completed: July 7, 2002, 10:19:19  
Job time: 271 sec

